


```
QY 241 AKNVMTLMLVYACVDVPRIVKALGEVNDGDLGANA VNVLDSEGNPLHHAANKCTGD 300
Db |||||
QY 256 AKNVMTLMLVYACVDVPRIVKALGEVNDGDLGANA VNVLDSEGNPLHHAANKCTGD 315
Db |||||
QY 301 KLKLCWEKTKTDIDITANFANQSPHLHIITQKPDSCVLDIEEFTSRNLDGGLVGDGKNPL 360
Db |||||
QY 316 KLKLCWEKTKTDIDITANFANQSPHLHIITQKPDSCVLDIEEFTSRNLDGGLVGDGKNPL 375
Db |||||
QY 361 HHAVEHLPPVILKGVMDHVNSSEFQDLVNDPDYFGNTIAHVA VKNKADLTFLNMLKAS 420
Db |||||
QY 376 HHAVEHLPPVILKGVMDHVNSSEFQDLVNDPDYFGNTIAHVA VKNKADLTFLNMLKAS 435
Db |||||
QY 421 GADLVNVRVGRAPIHVASSNGKANAVSLVSCGIDVNSQDVNGDTPHLHIAVEGSGMETV 480
Db |||||
QY 436 GADLVNVRVGRAPIHVASSNGKANAVSLVSCGIDVNSQDVNGDTPHLHIAVEGSGMETV 495
Db |||||
QY 481 LAVLNQRGADVSVQNNNDGVTTPMLSAKYGDIGVIRKALGSAKPNIKGEDTVAKSLMEDYK 540
Db |||||
QY 496 LAVLNQRGADVSVQNNNDGVTTPMLSAKYGDIGVIRKALGSAKPNIKGEDTVAKSLMEDYK 555
Db |||||
QY 541 GTPPLHFVAGGSRDTPFRVRKQNYEKCHDLATIRAAALMDQSGGELVNLGDFESENILGS 600
Db |||||
QY 556 GTPPLHFVAGGSRDTPFRVRKQNYEKCHDLATIRAAALMDQSGGELVNLGDFESENILGS 615
Db |||||
QY 601 PNAKFLQHIQSANFGSPARRGIVSSNNHNMKDIILNFVGDLSLHLPSERGYNAMQVAALFG 660
Db |||||
QY 616 PNAKFLQHIQSANFGSPARRGIVSSNNHNMKDIILNFVGDLSLHLPSERGYNAMQVAALFG 675
Db |||||
QY 661 DKEAVNMLAKSPKDLNFKTSATPTPLNACLARGDNEVVRGLVQGHGIDINQRMGSDKN 720
Db |||||
QY 676 DKEAVNMLAKSPKDLNFKTSATPTPLNACLARGDNEVVRGLVQGHGIDINQRMGSDKN 735
Db |||||
QY 721 TVLHVAISKDGFSLVQKILAHGTVDVNCENNIQOTPLHLAVEGDPKIVSSLLKAGAVN 780
Db |||||
QY 736 TVLHVAISKDGFSLVQKILAHGTVDVNCENNIQOTPLHLAVEGDPKIVSSLLKAGAVN 795
Db |||||
QY 781 RLDDNGRSVLSNAIVPGRKEKGVILGVNKLDRGADINLDGDHNLFDQCL 831
Db |||||
QY 796 RLDDNGRSVLSNAIVPGRKEKGVILGVNKLDRGADINLDGDHNLFDQCL 846
Db |||||
```

RESULT 2

```
Q8AX92
ID Q8AX92 PRELIMINARY; PRT; 1179 AA.
AC Q8AX92;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]_TaxID=31033;
RP SEQUENCE FROM N.A.
RA Kosan C., Kunz J.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF527754; AA015006.1; -.
DR HSSP; P55271; 1D9S.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 23.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 22.
DR PROSITE; PS50088; ANK_REPEAT; 16.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
SQ ANK repeat; Hypothetical protein.
KW SEQUENCE 1179 AA; 127675 MW; ABFF2F2B2CC14EF2 CRC64;

Query Match 10.3%; Score 442; DB 2; Length 1179;
Best Local Similarity 22.5%; Pred. No. 1.2e-15;
Matches 211; Conservative 102; Mismatches 310; Indels 34; Gaps 34;
```

RESULT 3

```
AN28_HUMAN
ID AN28_HUMAN STANDARD; PRT; 1059 AA.
AC O15084;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
```



```
DR HSSP; P16157; IN11.
DR GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR GO; GO:0005856; C:cytoskeleton; NAS.
DR GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
DR GO; GO:0019899; F:enzyme binding; ISS.
DR GO; GO:0030507; F:spectrin binding; ISS.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
DR GO; GO:0006887; F:exocytosis; NAS.
DR GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; Ank; 23.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 23.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR ANK repeat.
SQ SEQUENCE 1719 AA; 189010 MW; F63465D16D975CBF CRC64;

Query Match          9.1%; Score 390.5; DB 2; Length 1719;
Best Local Similarity 26.0%; Pred. No. 1.5e-12;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

QY 194 RIVASGKDLSEQVEIILIPWSEIEAGISNPLHADVDNPNVK-----GA---- 241
DB 194 RIVASGKDLSEQVEIILIPWSEIEAGISNPLHADVDNPNVK-----GA---- 241
DB 256 RLLDORGAGIEYTKDEL-----TPHCAARGHVRISILLDHGAPQA 300
QY 242 --KNVMTLHLYVACD--VDPRIYKALGEVNDGDLGANAYNVLDSEGNPLHHAAXNCT 298
DB 242 --KNVMTLHLYVACD--VDPRIYKALGEVNDGDLGANAYNVLDSEGNPLHHAAXNCT 298
DB 301 KTKNGLSPIHMAAQGHLD--CVRLLLQYDAEIDDI-----TLD---HLTPLHVAAGC 349
QY 299 GKLL-KLCEKTYTDFIDTANFANGSPHIIITQKDCSVLDIEEFTSRNLDGLVDGDK 357
DB 299 GKLL-KLCEKTYTDFIDTANFANGSPHIIITQKDCSVLDIEEFTSRNLDGLVDGDK 357
DB 350 HHRVAKVLLDKGAKPNRSLN--GFTPLHIACKNHRVMEILLKTGASID--AVTESGL 405
QY 358 NPLHIA--VEHLPPV---ILKGVMHDVKNSSFEQDLVNDPDYF---GNT-IAHVAVRNK 407
DB 358 NPLHIA--VEHLPPV---ILKGVMHDVKNSSFEQDLVNDPDYF---GNT-IAHVAVRNK 407
DB 406 TPLHVASFWGHLPIYKVLQORASPNVSVK-----VETPLHVAARAGHTEVAKYLLQNK 460
QY 408 NADLTFLNMLKASGADLVNRVYGRAPTHVASNGKANAVSLGIDVNSQDVNGDTP 467
DB 408 NADLTFLNMLKASGADLVNRVYGRAPTHVASNGKANAVSLGIDVNSQDVNGDTP 467
DB 461 -----AKVNAKAKDDQTPHCAARIGHNTNNVKKLENNANPNLATTAHTP 506
QY 468 LHIAVEGSGMETVLAVLNORGADVSNQNDGVTPLMSAAKYDGIKAL--GSAKPNIK 525
DB 468 LHIAVEGSGMETVLAVLNORGADVSNQNDGVTPLMSAAKYDGIKAL--GSAKPNIK 525
DB 507 LHIAAREGHVETVALL--EKEASQACMTKKGFTPLHVAAYKGVRYAELLERDAPNAA 565
QY 526 GEDTVAKSLMEDYKGTPLHFAVGGSRTDTRVVRKNYKCHDLATIRAAALMQDRSGGE 585
DB 526 GEDTVAKSLMEDYKGTPLHFAVGGSRTDTRVVRKNYKCHDLATIRAAALMQDRSGGE 585
DB 566 GKN-----GLTPLHVAHNNLDIVKL----- 587
QY 586 LVNLGDFESENTLGSPNAKPLQHIQSANFGSPARRGIVSSNNHVMKDIINLVGDSLHLP 645
DB 586 LVNLGDFESENTLGSPNAKPLQHIQSANFGSPARRGIVSSNNHVMKDIINLVGDSLHLP 645
DB 588 LLPRG-----GSP-----HSPAWN-GYTPHIAAQKQNEVARSLLQY-CGSANAE 631
QY 646 SERGYNAMQVALFGDKAEKVMKLSAKSPDLNFKTSATPTPLNLACLGDNENVRLVG 705
DB 646 SERGYNAMQVALFGDKAEKVMKLSAKSPDLNFKTSATPTPLNLACLGDNENVRLVG 705
DB 632 SVQGVTPHLAAQEGHAEVWALL--SKOANGNLGNKSLGTLPHLVAQEGHVPADVLI- 688
QY 706 QHG--IDINQRGSDKNTVHLVAISKGDSFLVKILAHTGVNDVNCNNLQGTPLHLAVBG 763
DB 706 QHG--IDINQRGSDKNTVHLVAISKGDSFLVKILAHTGVNDVNCNNLQGTPLHLAVBG 763
DB 689 KGVWVDATRMG--YTPHVAHYGNIKLVKFLQHQ--ADVNAKTKLGYSPLHQAQQ 744
QY 764 GPKIVSLLKAGAVNRLDDNGRSVLSAIVPGRKEKVLGVNKL----LDRGADINLD 820
DB 764 GPKIVSLLKAGAVNRLDDNGRSVLSAIVPGRKEKVLGVNKL----LDRGADINLD 820
DB 745 GHTDITVTLKNGASPNVSSDGTTPLAIA-----KRLGYISVTDVLKVVTDTSFVLVS 799
```

DR GO: 0005200; F: structural constituent of cytoskeleton; ISS.
 DR GO: 0045199; P: maintenance of epithelial cell polarity; ISS.

DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000488; Death.

DR InterPro: IPR011029; DEATH_like.
 DR InterPro: IPR000906; ZUS.

DR Pfam: PF00023; Ank; 22.
 DR Pfam: PF00531; Death; 1.

DR Pfam: PF00791; ZUS; 1.
 DR PRINTS: PR01415; ANKYRIN.

DR SMART: SM00248; ANK; 22.
 DR SMART: SM00005; DEATH; 1.

DR SMART: SM00218; ZUS; 1.
 DR PROSITE: PS50088; ANK REPEAT; 20.

DR PROSITE: PS50297; ANK REP REGION; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.

DR ANK repeat.
 KW ANK repeat.

SQ SEQUENCE 1856 AA; 203465 MW; 4A4E3A794DD6401F CRC64;

Query Match 9.1%; Score 390.5; DB 2; Length 1856;
 Best Local Similarity 26.0%; Pred. No. 1.6e-12;

Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

QY 194 RIVASKGDLSEQVEEILDIIFNNESEIAGISNPLHADVNNPVK-----GA----- 241
 DB 223 RLLDRGAQIETKTDEL-----TPHCAARNGHVRISSEILLDHGAPIQA 267

QY 242 --KNVMTLMHLVACD--VDPRIKALGEVENDEGLGANAYNVLDSGNPLPHAAKNCT 298
 DB 268 KTKNGLSPIHMAAGDHL--CVRLLOYDAEIDDI-----TLD-----HLTPHVAHCG 316

QY 299 GDKL-KLCMEKTKTDFIDTANFANQSPHLHIITQKPCDVLIDIEFTSRNLDLFGVDGDK 357
 DB 317 HHRVAKVLKDGAKPNSRALN--GFTPLHACKNHVRVVELLLKTGASID--AVTESGL 372

QY 358 NPLHHA--VEHLPPV-----ILKGMDHVKNSEFQDLVNDPDPF-----GNT-IAHYAVKNK 407
 DB 373 TPLHVASFMGHLPIVKNLQORGASPNVSNVK-----VETPLHMAARAGHTEVAKYLLQNK 427

QY 408 NADLTLPNMLKASGADLVNVRVGRAPIHVASSNGKANAYSGLVSCGIDVNSQDVNGDTP 467
 DB 428 -----AKVNAKAKDDQTPHCAARIIGHTNMVLLLENNANPLATTAGHTP 473

QY 468 LHIAVEGSGMETVLAVLNORGADVSVQNDGVTPLMLSAKYDGIQVICAL--GSAKPNIK 525
 DB 474 LHIAAREGHVETVLALL--EKEASQACWTCKGFTPLHVAAYKGVKRVVAELLERDAHPNAA 532

QY 526 GEDTVAKSLMEDYKGTPTPLHFVAGGSRDTFRVRKNYEKCHDLATIRAAALMQDRSGGE 585
 DB 533 GKN-----GLTPLHVAVHHNLDIVKL----- 554

QY 586 LVNLGDPESNILGSPNAKFLQHTQSANFGFSPARGIVSSNNHNMVKDILNPFVGDLSHLP 645
 DB 555 LTPRG-----GSP-----HSPAWN-GYTPHLHIAKONQVEVARSLLQY-GGSANAE 598

QY 646 SERGYNAMQVAALFGDKEAVKMLAKSAKPSDLNFKTSATPTPLNACLRLGDNEVRGLVG 705
 DB 599 SVQGVTPHLAAQEGHAEMVALL--SKQANGNLGNKSGLTPLHLVAQEGHPVADVLI- 655

QY 706 QHG--IDINRMGSKNNTVLHYAISKGDSPFLVKILAHGTGVNVCNNLQGTPLHLAVEG 763
 DB 656 KHGVMDVATRMG---YTPHLVASHVGNIKLVKVFLLQHQ--ADVNAKTKLGYSPLHQAAQ 711

QY 764 GDPKIVSSLLKAGAVNRLDNGRSVLSSAIVGRKEKGVILGVNKL---LDRGADINLD 820
 DB 712 GHTDI VLLKNGASPNVSSDGTTPLAIA-----KRLGVISVTDVLKVVTDTSFVLVS 766

QY 821 GDHNILFDQ 829
 DB 767 DKHMSFPE 775

RESULT 6

ANK1_HUMAN

ID ANK1_HUMAN

AC P16157;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).

GN Name=ANK1; Synonyms=ANK;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.

RC TISSUE=Hematopoietic;

RX MEDLINE=90158830; PubMed=2137557;

RA Lux S.E., John K.M., Bennett V.;

RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated

RT structure with homology to tissue-differentiation and cell-cycle

RT control proteins.";

RL Nature 344:36-42(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=90175370; PubMed=1699849;

RA Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,

RA Cheung M.C., Kan Y.W., Palek J.;

RT "cDNA sequence for human erythrocyte ankyrin.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).

RN [3]

RP VARIANT HS ILE-462.

RX MEDLINE=96225450; PubMed=8640229;

RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,

RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,

RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;

RT "Ankyrin-1 mutations are a major cause of dominant and recessive

RT hereditary spherocytosis.";

RL Nat. Genet. 13:214-218(1996).

CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal

CC elements; bind to the erythrocyte membrane protein band 4.2, to

CC Na-K ATPase, to the lymphocyte membrane protein GP85, and to the

CC cytoskeletal proteins fodrin, tubulin, vimentin and desmin.

CC Erythrocyte ankyrins also link spectrin (beta chain) to the

CC cytoplasmic domain of the erythrocytes anion exchange protein;

CC they retain most or all of these binding functions.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic surface of erythrocytic plasma

CC membrane.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Comment=Additional isoforms seem to exist;

CC Name=1; Synonyms=2.1;

CC IsoId=P16157-1; Sequence=Displayed;

CC Name=2; Synonyms=2.2;

CC IsoId=P16157-2; Sequence=VSP_000264, VSP_000265;

CC Name=3;

CC IsoId=P16157-3; Sequence=VSP_000266;

CC -1- PTM: Regulated by phosphorylation.

CC -1- PTM: Palmitoylated.

CC -1- DISEASE: Defects in ANK1 are a cause of hereditary spherocytosis

CC (HS) [MIM:182900]. Inheritance can be autosomal dominant or

CC recessive.

CC -1- SIMILARITY: Contains 23 ANK repeats.

CC -1- SIMILARITY: Contains 1 death domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X16609; CAA34610.1; -.

CC EMBL; M28880; AAA51732.1; -.


```
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR000906; ZUS.
DR Pfam: PF00023; Ank; 23.
DR Pfam: PF00531; Death; 1.
DR Pfam: PF00791; ZUS; 1.
DR PRINTS: PR01415; ANKYRIN.
DR SMART: SM00248; ANK; 23.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00218; ZUS; 1.
DR PROSITE: PS50088; ANK REPEAT; 20.
DR PROSITE: PS50297; ANK REP REGION; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW ANK repeat.
SQ SEQUENCE 1848 AA; 202576 MW; 5744BECBF9EBA056 CRC64;

Query Match      8.9%; Score 382.5; DB 2; Length 1848;
Best Local Similarity 26.2%; Pred. No. 4.5e-12;
Matches 180; Conservative 98; Mismatches 259; Indels 151; Gaps 33;

221 I AEGISNPLHADVDNPNVKGAKNVMTLMHLVYACDVDPRIKALGEVNDGDLGANAYN 280
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
156 LQQGHENVV-AHLINYGTKG-KVRLPALHIAARN-DTRTAAVL--LQNDPNP-----D 204
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
281 VLDSEGNLPLHAAKNCTGDKLCKWETKTFDITANFANO---SPLHIITQKDCSVL 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 VLSKTGFTPLHIAAHYENLNVAQLLNKGA-----SVNFTPQNGITPLHIASRGNVIMV 259
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
338 DI-----EEFT-----GRN-----LDPG-----LVDGDKNPLHHA--- 363
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
260 RLLDRGAQIETRTKDELTPHCAARNGHVRISILLDHGAPIQAKTNGLSPIHMAAQG 319
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
364 -----VHLPVILKGMVDHVKNSSSEPDQVNDPDP-----YEGNTIA 400
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
320 DHLDCVRLQLQNAEIDITDLHPLHVAACHGHRVAKVLLDKGAKPNSRALNGFTPL 379
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
401 HYAVKKNKADLTFLNMLKSGADLVNVRNVGRAPITHVASSNGKANAVSLVSCGIDVNSQ 460
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
380 HIAKQNH--IRWMLLTKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVS 437
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
461 DVNGDTPLHIAVEGSGMETVLAVLNQRGADVSVQNNQDGVTPMLSAKYGDIGVIAL--G 518
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
438 NVKVTETPLHMAARAGHTE-VAKYLLQNKAKAKAKADQOTPLHCAARIGTGMVKLLLEN 496
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
519 SAKPNI-----KGEDTVAKSLMED-----YKGTPLHFAVAGGSRDTF 557
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
497 GASPNIATTAGHTPLHTAAREGHVDLTALLEKEASQACMTKKGFTPLHVAAYK--V 553
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
558 RYVRKNYKCHD-----LATIRALMQDRGGELVNLGDPFESENIL----GSPNAK 604
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
554 RLAEILLE--HDAHFNPAAGKNGITPLHVAVHNHL--DIVKL-----LLPRGSGP--- 599
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
605 FLOHTQSANFGSPARRGIVSNHNVMKDILNFVGSLSLHPSERGVNMQVAALFGDKXA 664
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
600 ---HSPAWN-GVTPHIAAKQNIQIEVARSLQY--GGSANAEVSQGVTPHLHAAQEGHTEM 654
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
665 VKMLAKSAKPSDLNFKTSATPTPLNLACLRGNEVVRGLVGQHG--IDINQRMGSDKQTV 722
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
655 VALLL--SKQANGNLGNKSGLTPLHLVSOEGHPVPADVLI-KHGVTVDTATRMG---YTP 708
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
723 LHVATSKGDSFLVQKITLAHTGVVDVNCNNLGTOTPLHLAVEGGDPKTVSLLLKAGAVNRL 782
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
709 LHVASHYGNIKLVKFLQHQ-ADVNAKTKLGVSPHLHQAQQGHTDITVILLKNGASPNREV 767
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
783 DNGRSVLSSAIVPGKEKGVILGNKL 810
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
768 SSGTTPPLAIA-----KRLGYISVTDVL 790
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
ANK1_MOUSE
ID ANK1_MOUSE STANDARD; PRT; 1862 AA.
AC Q02357;
DT 01-NOV-1995 (Rel. 32, Created)
```

```
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ankyrin 1 (Erythrocyte ankyrin).
GN Name=Anki; Synonyms=Ank-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RA MEDLINE=92345717; PubMed=1386265;
RX White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
    regulatory domain.";
RL Mamm. Genome 3:281-285(1992).
CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
    elements; bind to the erythrocyte membrane protein band 4.2, to
    Na-K ATPase, to the lymphocyte membrane protein gp85, and to the
    cytoskeletal proteins fodrin, tubulin, vimentin and desmin.
    Erythrocyte ankyrins also link spectrin (beta chain) to the
    cytoplasmic domain of the erythrocytes anion exchange protein;
    they retain most or all of these binding functions.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic surface of erythrocytic plasma
    membrane.
CC -!- PTM: Regulated by phosphorylation (By similarity).
CC -!- PTM: Acylated by palmitic acid group(s) (By similarity).
CC -!- SIMILARITY: Contains 23 ANK repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch)
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DR EMBL; M84756; AAA37236.1; -.
DR F1R; I49502; I49502.
DR HSSP; P16157; IN11.
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DR GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
DR GO; GO:0019899; F:enzyme binding; ISS.
DR GO; GO:0030507; F:spectrin binding; ISS.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
DR GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
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DR SMART; SM00248; ANK; 23.
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FT DOMAIN 1 827
FT DOMAIN 828 1386
FT DOMAIN 1387 1862
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FT REPEAT 73 102
FT REPEAT 106 135
FT REPEAT 139 168
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DR EMBL; L40632; AAB01606.1; -.
DR EMBL; L40631; AAB01602.1; -.
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DR PIR; T42714; T42714.
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DR PIR; T42716; T42716.
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FT DOMAIN 23 810 24 X ANK MOTIF REPEATS.
FT DOMAIN 856 1437 SPECTRIN BINDING DOMAIN.
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FT REPEAT 56 88 ANK MOTIF 2.
FT REPEAT 89 121 ANK MOTIF 3.
FT REPEAT 122 154 ANK MOTIF 4.
FT REPEAT 155 183 ANK MOTIF 5.
FT REPEAT 184 216 ANK MOTIF 6.
FT REPEAT 217 249 ANK MOTIF 7.
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FT REPEAT 283 315 ANK MOTIF 9.
FT REPEAT 316 348 ANK MOTIF 10.
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FT REPEAT 646 678 ANK MOTIF 20.
FT REPEAT 679 711 ANK MOTIF 21.
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FT VARSPLIC 1 849 Missing (in isoform 2 and isoform 3).
/FTId=VSP_050350.
FT VARSPLIC 833 853 Missing (in isoform 7 and isoform 8).
/FTId=VSP_050351.
FT VARSPLIC 834 855 VKASAPKLSGDEVISDGEEG -> GDKCTWFKIPKQEV
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/FTId=VSP_050352.
FT VARSPLIC 850 855 SDGEEG -> MALPHS (in isoform 2 and
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FT VARSPLIC 852 852 G -> GDKCTWFKIPKQEVLVKS (in isoform 4
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/FTId=VSP_050354.
FT VARSPLIC 1569 1764 Missing (in isoform 3, isoform 4 and
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FT SEQUENCE 1943 AA; 212013 MW; B23C4B6F82904804 CRC64;

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Best Local Similarity 25.7%; Pred. No. 8e-12; Indels 133; Gaps 27;
Matches 175; Conservative 98; Mismatches 275;

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DB 180 TKGKVRLPALHIAARKDD-----TKAAALLQNDTNADVESKSGFT-PLHIAAHYGNIN 232
QY 231 -----ADVNNPVKAGKQNMVTLMLVYACVDVDPRIKVALGEVENDEGLGANAYNV 281
DB 233 VATLLNRAAAVDFT---ARNDITPLH-VASKRGNANMVKLL-----LDRGAK-IDA 279
QY 282 LDSEGNLPHHAAKNCCTGDKLKCWEKTKDFTDITANFANOSPLHIITQKPDSCVLDIEE 341
DB 280 KTRGLTPLHCGARSHEQVVMELDRSAPILSKTKN--GLSPLHMAFGDHLNCVQJ--- 335
QY 342 FTSRNLDGFLVDGDKNPLHHAHVEHLPPVILKGYMDHVKNSSSEFQDLVNDPDYFGNTIAH 401
DB 336 LLQHNVPVDDVTNDYLTALHVAACHGHYKVAKVLLD--KKASPNAKALN-----GFTPLH 388
QY 402 YAVNKNADLTFLNMLKASGADLNVRNVVGRAPIHVASSNGKANAVSLVSCGIDVNSQD 461
DB 389 IACK-KNR-IRVMELLKKGASIQAVTESGLTPIHVAAFMGHVNIVISQLMHHGASPNNTN 446
QY 462 VNGDTPLHIAVEGGSGMETVLAVLNORGADYSVQNNDGVTPLMSAAKYGDIGIKAL--GS 519
DB 447 VRGETALHMAARSQAEB--VRYLVQDGAQVEAKAKDDQTPLIHSARLGKADIVQQLQOG 505
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DB 506 ASPNAATTSGYTPHLAAREGHEDVAFLLDHGASLSITTKKGTPLHVAAYKGLV-- 563
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DB 642 AVTRQGIASVHLAAQEGHVDVMSLLSRNANVNLNKSGL---TPLHLA-AQEDRVNVAE 697
QY 738 ILAHTGVDVNCENNLGQTPHLHAVEGGDPKIVSVLSLLKAGAVVNRLLDNGRSVLSSAIVPG 797
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DB 754 -AQQGHTHIINVLLQNNASPN 773

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ankyrin 3 (ANK-3) (Ankyrin G).
GN Name=ANK3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Brain stem;
RX MEDLINE=95138209; PubMed=7836469; DOI=10.1074/jbc.270.5.2352;
RA Kordeli E., Lambert S., Bennett V.;
RT "AnkyrinG. A new ankyrin gene with neural-specific isoforms localized

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at the axonal initial segment and node of Ranvier.";
 J. Biol. Chem. 270:2352-2359(1995).
 CC -1- FUNCTION: Membrane-cytoskeleton linker. The neural-specific
 isoforms may participate in the maintenance/targeting of ion
 channels and cell adhesion molecules at the nodes of Ranvier and
 axonal initial segments.
 CC -1- SUBUNIT: Neural-specific isoforms may be a constituent of a
 neurofascin/NRCAM/ankyrin G complex.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoform=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1; Synonyms=480-Kda isoform;
 CC IsoId=Q12955-1; Sequence=Displayed;
 CC -1- TISSUE SPECIFICITY: Expressed in brain and other tissues. Isoform
 1 is neural-specific.
 CC -1- SIMILARITY: Contains 23 ANK repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
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EMBL; U13616; AAA64834.1; --
 DR PIR; A55575; A55575.
 DR HSP; P16157; IN11.
 DR Genew; HGND:494; ANK3.
 DR MIM; 600465; --
 DR GO; GO:0006605; P:protein targeting; NAS.
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 DR InterPro; IPR011029; DEATH_like.
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 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00791; ZU5; 1.
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 FT DOMAIN 1519 1898 Ser-rich.
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 QY 342 FTSRNLDGLVDGDKNPLHVAHEHLPVILKGVMDHVNSEFQDLVNDPDPFGNTIAH 401
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 DB 464 VRGETALHMAARSGQAE-VVRYLVODGAQVEAKAKDDQTFPHISARLGRKADI VOQLLQOG 522
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 QY 615 GFSPARRGIVSSNNHNMKDI LNFVGDLSLHPSERGYNAMQVAFDGEKAVKMLAKSAP 674
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 QY 675 SDLNFKTSATPTPLNLACLRGDNVVRGLVQGH-GIDINQRMGSKNTVLHYAISKGDSE 733
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 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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 RC STRAIN=breed Japanese Black; TISSUE=Bone marrow;
 RA Matsumoto M., Inaba M., Koshino I., Saito D., Ono K.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF222766; AAF61702.1; -.
 DR HSSP; P16157; IN11.
 DR InterPro; IPR002110; ANK.

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
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 RA Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
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 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
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 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
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 RA Ashburner M., Celnik S.E.;
 RA "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celnik S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
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 RT "A Drosophila mechanosensory transduction channel.";
 RL Science 0:0-0(2000).
 DR EMBL; AF003609; AAF52248.3; -;
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 DR InterPro; IPR000345; CytC_heme_BS.
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 DB 77 RDTANKVLG-LAMKSEWTPIEAEKKL-EKYVANVE----- 111
 QY 225 ISNPLHADVDNNPVGAKNVT-LMHLVYAC-DVDPRIVKALGEVNDDEGLCANAYVL 282
 DB 112 -----DGNHPIPLAGVHDMNTGMTPLMYATKDKNTAIMDRMIELGADVGGARNNDNNV- 163
 QY 283 DSEGNLPLHHAANKCTGDKLCKMEKTKTDIDTANFANQSPHLHITOKPCSVLIDIEB- 341
 DB 164 -----LHIAAMYSREDVVKLLITKRGVDPFSTGSSRSQTAVHLVSSRQTGTATNILRA 216
 QY 342 -FTSRNLDPLGL-VDGDGNPLHHAHVEHLPPVILKGVMDHVKNSSSEFQDLVNDPDYFGNTI 399
 DB 217 LLAAGKDIRLKADGRGKIPLLAVESGNQSMCRELL-----AAQTAQLKATTANGDTA 271
 QY 400 AHYAVKKNADLTILFNMLKASGADLVNRNVVGRAPIHVASSNGKANAVSLVSCGIDVNS 459
 DB 272 LHLAARRDDVMV--RILVDYGTNVDTQNGEGQTPHLIAAAEGDEALKYFYGVSRASASI 329
 QY 460 QDVNGDTPHLHTAVGSGSMETV-----LAVLV-----Q 486
 DB 330 ADNQDTPMHLAAENGHANHVETIILADKPKASIFERTKDGSTLMHIASLNGHAECATMLPK 389
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 DB 450 VETLLGFGADVHVVRGGKLRET-----PLHTAARVKDGRCALMLLKSGASPNLTDT 500

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OM protein - protein search, using sw model

Run on: February 26, 2005, 18:36:06 ; Search time 174 Seconds
(without alignments)
1847.114 Million cell updates/sec

Title: US-10-701-038-2

Perfect score: 4310
Sequence: 1 PSGDIQSQSQDQEQDQQ.....DRGADINLDGHNILFDQCL 831

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4310	100.0	831	8	ADO15511 Immunorea
2	1963	45.5	390	5	ADG31916 E canis p
3	1300.5	30.2	831	8	ADO15510 Immunorea
4	421	9.8	1053	4	AAU28174 Novel hum
5	421	9.8	1059	7	ADK65850 Angiogene
6	421	9.8	1059	8	ADK658330 Human pro
7	413	9.6	705	4	AAU20496 Human sec
8	391.5	9.1	1880	8	ADR90358 Full leng
9	390.5	9.1	1881	7	ADK47763 Human pro
10	382.5	8.9	899	8	ABM80426 Tumour-as
11	382.5	8.9	1536	6	ABU11523 Human MDD
12	377.5	8.8	4274	4	ABG00972 Novel hum
13	377.5	8.8	4386	4	ABG07375 Novel hum
14	373.5	8.7	687	8	ADR08749 Human pro
15	373.5	8.7	1056	6	AAE33684 Human str
16	370.5	8.6	994	7	ADK65799 Angiogene
17	370.5	8.6	1012	7	ADK65847 Angiogene
18	370	8.6	1619	4	AAU00986 Drosophil
19	368.5	8.5	1330	7	ADM04552 Human pro
20	368.5	8.5	1839	7	ADD27862 Human bra
21	368.5	8.5	1872	4	AAU79160 Human pro
22	368.5	8.5	2622	7	ADK65508 Rat Prote
23	368.5	8.5	4397	4	ABG21944 Novel hum
24	368	8.5	1619	4	AAU00970 Drosophil
25	366.5	8.5	1619	4	AAU00988 Drosophil

26 364.5 8.5 919 7 ADM05437 Human pro
27 363.5 8.4 1619 4 AAU00987 Drosophil
28 363.5 8.4 1954 8 ABM83918 Human dia
29 363.5 8.4 1955 8 ABM83917 Human dia
30 363.5 8.4 3897 8 ABM83919 Human dia
31 363.5 8.4 3924 8 ABM83916 Human dia
32 363.5 8.4 3955 8 ABM83915 Human dia
33 363.5 8.4 3985 8 ABM83914 Human dia
34 363.5 8.4 4016 8 ABM83912 Human dia
35 363.5 8.4 4072 8 ABM83913 Human dia
36 363.5 8.4 4082 8 ABM83911 Human dia
37 362.5 8.4 1003 8 ADS10956 Human the
38 358 8.3 1076 8 ADQ66099 Novel hum
39 355.5 8.2 843 7 ADD27861 Rat ankyr
40 351 8.1 1709 4 AAU00971 Caenorhab
41 350 8.1 1088 4 AAB62429 Human kid
42 350 8.1 1094 6 AAE33688 Human str
43 350 8.1 1097 4 ABG21941 Novel hum
44 349.5 8.1 1453 4 ABB65398 Drosophil
45 348.5 8.1 1118 8 ADS10993 Human the

ALIGNMENTS

RESULT 1
ADO15511
ID ADO15511 standard; protein; 831 AA.
XX AC ADO15511;
XX AC ADO15511;
DT 12-AUG-2004 (first entry)
XX AC ADO15511;
DE Immunoreactive surface protein p156, SEQ ID 2.
XX AC ADO15511;
KW Vaccine; immunoreactive; surface glycoprotein; p153; p156;
KW canine ehrlichiosis; human ehrlichiosis.
XX AC ADO15511;
OS Ehrlichia chaffeensis.
XX AC ADO15511;
PN WO2004042037-A1.
XX AC ADO15511;
PD 21-MAY-2004.
XX AC ADO15511;
PF 04-NOV-2003; 2003WO-US034916.
XX AC ADO15511;
PR 04-NOV-2002; 2002US-0423573P.
XX AC ADO15511;
(RERE-) RES DEV FOUND.
XX AC ADO15511;
PI McBride JW, Walker DH;
XX AC ADO15511;
DR WPI; 2004-419705/39.
XX AC ADO15511;
PT New DNA encoding Ehrlichia species immunoreactive surface protein p153 or
PT protein p156, useful as vaccines against canine and human ehrlichioses or
PT for diagnosing ehrlichioses.
XX AC ADO15511;
PS Claim 6; SEQ ID NO 2; 41pp; English.
XX AC ADO15511;
CC The present invention relates to Ehrlichia canis immunoreactive surface
CC glycoprotein p153 (ADO15510) and Ehrlichia chaffeensis immunoreactive
CC surface glycoprotein p156 (ADO15511). The proteins are useful as subunit
CC vaccines against canine and human ehrlichioses. They are also useful for
CC serologic and molecular diagnostics of E. canis or E. chaffeensis.
XX AC ADO15511;
SQ Sequence 831 AA;

Query Match 100.0%; Score 4310; DB 8; Length 831;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGDIQSQSQDQEQDQQGAVGVGNSPIERVAAPESDLYTVIIPKGRKTAAP 60

AC ADO15510; ;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Immunoreactive surface protein p153, SEQ ID 1.
 XX
 XX Vaccine; immunoreactive; surface glycoprotein; p153; p156;
 KW canine ehrlichiosis; human ehrlichiosis.
 KW
 XX Ehrlichia canis.
 OS
 XX
 XX WO2004042037-A1.
 PN
 XX
 PD 21-MAY-2004.
 XX
 XX 04-NOV-2003; 2003WO-US034916.
 XX
 XX
 XX 04-NOV-2002; 2002US-0423573P.
 PR
 XX
 XX (HERE-) RES DEV FOUND.
 PA
 XX
 XX McBride JW, Walker DH;
 PI
 XX
 XX WPI; 2004-419705/39.
 DR
 XX
 XX New DNA encoding Ehrlichia species immunoreactive surface protein p153 or
 PT protein p156, useful as vaccines against canine and human ehrlichiosis or
 PT for diagnosing ehrlichiosis.
 XX
 XX
 XX Claim 12; SEQ ID NO 1; 41pp; English.
 PS
 XX
 XX The present invention relates to Ehrlichia canis immunoreactive surface
 CC glycoprotein p153 (ADO15510) and Ehrlichia chaffeensis immunoreactive
 CC surface glycoprotein p156 (ADO15511). The proteins are useful as subunit
 CC vaccines against canine and human ehrlichiosis. They are also useful for
 CC serologic and molecular diagnostics of E. canis or E. chaffeensis.
 XX
 XX Sequence 831 AA;
 SQ
 Query Match 30.2%; Score 1300.5; DB 8; Length 831;
 Best Local Similarity 35.7%; Pred. No. 1.6e-92;
 Matches 297; Conservative 156; Mismatches 265; Indels 113; Gaps 16;
 39 APSEDLTYVIIIPKGRTA-APILERKSPTEPKVEDDELDPTLPRTFSGE----- 90
 DB 11 AVEEDPLXAVLPKQRPAPTQVLEB-----DSVEEIEIAPLPNNVGEVEQEDP 65
 QY 91 -----GY-----DDGVSMPTVSR-----GIYQPPIVQDS-----NLY---SSIGGVP 125
 DB 66 IYQGIPOHQBEMEDPYASLDQVSQAGADGIQENPVPQAGRELEBDIYQDPADFGGLG 125
 QY 126 QEA-QYDAAARAG---GPRKFLYGYTFNSQIMDFEPTPWPVYRNALVGNKEIKEW 181
 DB 126 QGGQQLDQAGYQPSIGDRQLVNGPYGFNDGSYAMEFD-DVMWEGVRDAVIHDEEDPKF 184
 QY 182 LTTSQGVROIADRIKASGDLSDQVEEILDIIFMNESEIAEGISNPLHADVNNPVKGA 241
 DB 185 LVTDGLMRHICDKIVQSEGNLPEDLEEIVSLKNDKEGISELINEPQVVDIIFNNPVREG 244
 QY 242 KNYMTLHLVYACDVPRIKALGEVNEDEGLGANAYNVLDSEGNLPLHHAAKNCTGDK 301
 DB 245 RNVTMLHLAYAVNVDPRINAIESVNSFSGSLDGYNIQDADGNLPLHHAACNCGQV 304
 QY 302 LKLCMEKTKTDFDTANFANQSLPHIITQKPCDSCVLIDIEFTSRNLDGFLVD-GDGKNPL 360
 DB 305 LDNCISKTSNIINIRNFGNSQLPVMVQNPQSGSIGNIQVANECDGDFNLIDHPTGRMEI 364
 QY 361 HHAVEHLPPVILKGVMDHVNKSEFQDLVNDPFGNTIAHYAVKKNADLTILFNNLKAS 420
 DB 365 HYAAE-----AASE-----VLSYVIRTKAE----- 386
 QY 421 GADLNVRNVGRAPTHVANSNGKANAVSLVSCGIDVNSQDVGNDPTPLHIAVEGGSMETV 480

DB 387 -----SPQASA-----VNTQDVNGRTPLHCAAISGNSKGL 416
 QY 481 LAVLNORGADVSVQNNNDGVTPLMLSAKYGDIGVIKALGSAKPNIKGEDTVAKSLLMEDYK 540
 DB 417 SVMLLQNGVDCAVRDKNYSTPLHYAVAGNDIKIKNLCSVKRGVQGVKSSAAALLCEDLQ 476
 QY 541 GFTPLHFVAGGSRDTRFVRVKNYKCHDLATIRAALMQDRSGGELVNLGDFESENILGS 600
 DB 477 GDTPLHACKVEGTAKAFETVRQSIKKGHGKQVQLLEIREGSGPRL-NVSGFGSQSLISG 535
 QY 601 PHAKFLOHQSANFGSPARRGIVSSNHNVMKDILNFVGDLSLHPSERGNAMQVAAALFG 660
 DB 536 VSGDLYGYLNSQNFPTSPVHAAVKANNLQLNLFLKXSPDILKQSSPENGPNPVHMAALFA 595
 QY 661 DKEAVQMLAKSAKPSDLNFKTSATPTPLNLACLRGNEVVVRGLVGQHGIDINORMGSDKN 720
 DB 596 DVKTVKLIENASGEVNAQSDSTLPLHLACIRGDSIIKRMVEHESVNVNMTMPDQN 655
 QY 721 TVLHYAISKSDSFLVQKILAHTGVQVNCENNIGQTPHLHAVEGGDPKIYSSLLKAGAVVN 780
 DB 656 TVLQYAINRGHSLIKRLLSHPSIDLNVNRNADKTSASAMEKGDLLKTKVLCNAGADV 715
 QY 781 RLDDNGRSVLSSAIVPGRKEKGVGLGIWKLDRGADINLDGHNILFDQCL 831
 DB 716 TVDNGRSVISAISYSGQNEKLVPIVKLLNSGAKIGSQEDKNILLQKCI 766
 RESULT 4
 AAU28174
 ID AAU28174 standard; protein; 1053 AA.
 XX
 XX AAU28174;
 AC
 XX
 XX 18-DEC-2001 (first entry)
 DT
 XX
 DE Novel human secretory protein, Seq ID No 343.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 XX WO200166689-A2.
 PN
 XX
 PD 13-SEP-2001.
 XX
 XX 05-MAR-2001; 2001WO-US004942.
 PF
 XX
 XX 07-MAR-2000; 2000US-00519705.
 XX
 PR 19-MAY-2000; 2000US-00574454.
 PR 17-JUN-2000; 2000US-00596193.
 PR 14-JUL-2000; 2000US-00616847.
 PR 19-SEP-2000; 2000US-00665363.
 PR 20-OCT-2000; 2000US-00693267.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 XX WPI; 2001-589934/66.
 DR N-PSDB; AA845074.
 DR
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders.

XX	PS	Query Match	9.8%; Score 421; DB 4; Length 1053;
XX	CC	Best Local Similarity	25.2%; Pred. No. 2.1e-23;
XX	CC	Matches 189; Conservative 101; Mismatches 269; Indels 190; Gaps 29;	
CC	CC	The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (II) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention	
XX	CC	Sequence 1053 AA;	
XX	CC	Query Match 9.8%; Score 421; DB 4; Length 1053;	
XX	CC	Best Local Similarity 25.2%; Pred. No. 2.1e-23;	
XX	CC	Matches 189; Conservative 101; Mismatches 269; Indels 190; Gaps 29;	
Qy	Db	170	AVLGNKEIKE-----EWLTTSGPVRDIADIRIVASKGDLSEDQVEEILDIIF 215
Db	Db	49	AYLGDAEIIELLTILSGARVNAKDSKLT--PLH---RAVASCS-----EEAVQVLL 94
Qy	Db	216	MNESEIATGISN---PIHADVNNPVKGAKNVMTLMHLVYACDVPFRIVKALGEVNEDEG 272
Db	Db	95	KHSADVNAKDKNQWTPLHTAAANKAVKCAEALVPLLSNV----- 133
Qy	Db	273	DLGANAYNLDSGNPLHAAKNCCTGDKLCKMCKTKTDFDTANFANQSPHLIIITQKP 332
Db	Db	134	-----NVSDRAGRALTALHHAAPSGHGEVNVKLLSRGAN--INAFDKDRAIRHAAWYMG 184
Qy	Db	333	DCSVLDIEFTSRNLDFGLVDGDKNPLHAEVHLPVILKGMVDHVKNSSEFQDLVNDP 392
Db	Db	185	HIEVVKL--LVSHGAETVCKDKSYTPHAAAS-----SGNISVVKYLLDGLVDMNEP 235
Qy	Db	393	DYFGNTIAHYAVQKNADLTFLNMLKASGADLNVRNVVGRPIH-VASSNGKANAVSGVL 451
Db	Db	236	NAYGNTPLHVACYN-QQDVVV-NELIDCGAIVNQKNEKFTPLHFAAASATHGALCLELV 293
Qy	Db	452	SCGIDVNSQDVNGDTPLHTAIVEGSMETVLAVLNQEGADVSVQNNDGVTPLMSAAKYGI 511
Db	Db	294	GNAGDVNMKSQKGTPLHMTALHGRFSRSQTTI-QSGAVIDCEDKNGNTPLHIAARYGHE 352
Qy	Db	512	GVTKALGSAPNKGEDITVAKSLIMEDYKGFTHFVAGGSGRDTFRVVRKNYKEXCHDLA 571
Db	Db	353	LLINTLITS-----GADTAKRGI-----HGMPLHLAALSGFSD---CCRKLLSSGFID 399
Qy	Db	572	TI-----RAALMQDRSGELVLNGDFESENILGSPNAKFLQHTQSANQFGSPARRGIVSN 627

CC one of the differentially expressed proteins of the invention.

XX Sequence 1059 AA;

Query Match 9.8%; Score 421; DB 7; Length 1059;
 Best Local Similarity 25.2%; Pred. No. 2.2e-23;
 Matches 189; Conservative 101; Mismatches 269; Indels 190; Gaps 29;

QY 170 AVLGKKEIKE-----EWLTSGPVVDIADRVASKGDLSEDOVEILDIIF 215
 DB 55 AYLGDABIIELLILSGARVNKOSKWLTL---PLH-----RAVASC-----BEAVQVLL 100

QY 216 MNESEIAEGISN---PLHADVDNNPVKGAKNVMTLMHLVYACDVDPRIKALGEVENDEG 272
 DB 101 KHSADVNRDKNWQTPHLHAAANKAVKCAEALVPLLSNV----- 139

QY 273 DLGANAYNVLDSEGNPLHHAANKCTGDKLCKWTKTDFIDTANFANOSPLHIITQKP 332
 DB 140 -----NVSDRAGRTHLHAAAFSGHGMVKLLLSRGAN--INAFDKKORRAIHWAAVMG 190

QY 333 DCSVLDIIEFTSRNLDGFGDKGNPLHHAHVEHLPVILKGVMDHVKNSSSEFQDLVNDP 392
 DB 191 HIEVVKL--LVSHGAEVTCCKKSYTPLHAAAS-----SGMISVVKYLLDGLGVDMNEP 241

QY 393 DYFGNTIAHYAVKKNKADLTFLNMLKASGADLVNRVNVGRAPTH-VASSNGKANAVSGLV 451
 DB 242 NAYGNTPLHVACYN-GQDVVV-NELIDCGAIVNQKNEKGTPLHFAAASHTGALCLELLV 299

QY 452 SCGIDVNSQVNGDTPLHIAVEGSGMETVLAVLNQRGADVSVQNNQDVTPLMSAAKVDI 511
 DB 300 GNGADVNMKSKDGKTPHMTALHGRFSRSQTII-QSGAVIDCEDKNGNTPLHIAARYGHE 358

QY 512 GVTKALGSAKPNIKGEDTVAKSLMEDYKGTPLHFVAGGSRDTPRVVRKNYKCHDLA 571
 DB 359 LLINTLITS-----GATKARGI-----HGMFPLHLAALSGFSD---CCRLLSSGFDID 405

QY 572 TI-----RAALMQDRSGELVNLGDFESENTILGSPNAKFLQHIQSANFGSPARRGIVSSN 627
 DB 406 TPDDFGRTCLHAAAAGNL-----ECLNLLNTGADF---NKKDKFGRSPLHYAANCN 456

QY 628 HNVKDIILN---FVGD-----SLH-----LPSRGTNMQ 654
 DB 457 YDCLFALVSGASVNDLDERGCTPLHYAATSDTGKLEYLLRNDANPGIRDQGYNAHV 516

QY 655 VVALFGDKAEVKMLAKSPDLNFKTS-----ATPTPLNLAELRGNEVVRGL 703
 DB 517 YSAYGHURLCLQIIA-SETPLDMETSGTMDLSDSNRATISPLHIAAVHGHQALEVL 575

QY 704 VQGHGIDINORMGSD-----KNTVLHYAISKG 730
 DB 576 V-QSLDLDRVNSSGRTPDLAFAKGVHVCVDVLIHQGASILVKDYILKTPHIAAATNG 634

QY 731 DSFLVQKILAH-----TGVDVNCENNLGOTPLHIAVEGGDPKIVSSLLKAGAVNRLLDNG 786
 DB 635 HSECLRLLIAGNAEPQNAVDIQDGN--GQTPLMLSVLNGHTDCVYSLINKGANVDAKDKWG 692

QY 787 RSVLSSAIVPGRKEKGVGLVNVKLLDRGA 815
 DB 693 RTALHARGAVTCHEE-----CVDALLQHA 716

RESULT 6

ID ADS88330

XX ADS88330 standard; protein; 1059 AA.

AC ADS88330;

XX 18-NOV-2004 (first entry)

DT Human protein of a TNF-alpha signalling pathway protein complex Seq 185.

DE protein complex; tumour necrosis factor-alpha signalling pathway;

XX TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;

KW inflammatory bowel disease; infectious disease; septic shock;
 KW bacterial infection; neurological disease; stroke-induced inflammation;
 KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
 KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
 OS Homo sapiens.
 PN WO2004035783-A2.
 PD 29-APR-2004.
 XX 24-SEP-2003; 2003WO-EP050655.
 XX 26-SEP-2002; 2002EP-00021809.
 PR 10-FEB-2003; 2003EP-00100274.
 XX (CELL-) CELLZONE AG.
 PA Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
 PI Superti-Furga G, Kruse U;
 PI WPI; 2004-348460/32.

XX New protein complex comprising at least one first and second protein of

PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for

PT diagnosing or treating inflammation, neurological diseases, infectious

PT diseases or cancer.

XX Example; SEQ ID NO 185; 1980pp; English.

XX This invention relates to novel protein complexes of the tumour necrosis

CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to

CC methods for preparing these complexes comprising at least two component

CC proteins, as well as screening methods to identify modulators of the

CC pathway, which include antibodies, agonists and antagonists thereof. The

CC present invention describes a protein complex and kit that are useful for

CC diagnosing, prognosing or treating chronic inflammatory diseases such as

CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases

CC such as septic shock and bacterial infections; neurological diseases such

CC as stroke-induced inflammation in neurons; neurodegenerative diseases and

CC cancer. Accordingly, these complexes can be used for the development of

CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,

CC antirheumatic, cytostatic and antibacterial activities and can be used

CC for gene therapy purposes. In particular, the invention further provides

CC siRNA-oligonucleotides useful for inhibiting protein expression in in

CC vitro or cell culture assays. This polypeptide is a human protein that

CC can be used in combination with other proteins provided in the

CC specification to form novel complexes of the TNF-alpha signalling pathway

XX of the invention.

XX Sequence 1059 AA;

Query Match 9.8%; Score 421; DB 8; Length 1059;

Best Local Similarity 25.2%; Pred. No. 2.2e-23;

Matches 189; Conservative 101; Mismatches 269; Indels 190; Gaps 29;

QY 170 AVLGKKEIKE-----EWLTSGPVVDIADRVASKGDLSEDOVEILDIIF 215

DB 55 AYLGDABIIELLILSGARVNKOSKWLTL---PLH-----RAVASC-----BEAVQVLL 100

QY 216 MNESEIAEGISN---PLHADVDNNPVKGAKNVMTLMHLVYACDVDPRIKALGEVENDEG 272

DB 101 KHSADVNRDKNWQTPHLHAAANKAVKCAEALVPLLSNV----- 139

QY 273 DLGANAYNVLDSEGNPLHHAANKCTGDKLCKWTKTDFIDTANFANOSPLHIITQKP 332

DB 140 -----NVSDRAGRTHLHAAAFSGHGMVKLLLSRGAN--INAFDKKORRAIHWAAVMG 190

QY 333 DCSVLDIIEFTSRNLDGFGDKGNPLHHAHVEHLPVILKGVMDHVKNSSSEFQDLVNDP 392

DB 191 HIEVVKL--LVSHGAEVTCCKKSYTPLHAAAS-----SGMISVVKYLLDGLGVDMNEP 241

QY 393 DYFGNTIAHYAVKKNKADLTFLNMLKASGADLVNRVNVGRAPTH-VASSNGKANAVSGLV 451

or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1881 AA;

Query Match 9.1%; Score 390.5; DB 7; Length 1881;
Best Local Similarity 26.0%; Pred. No. 1.3e-20;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

QY 194 RIVASKGDLSEDOVEETLIDIFWNESEIARGISNPLHADVDNNPVK-----GA----- 241
DB 256 RLLDRAQALETYKDEL-----TPHCAARNGHVRSEILLDHGAPIQA 300
QY 242 -KNVMTLHVLVACD-VDPRIKALGEVDEGDLGANAYNVLDSEGNLPLHAAKNCT 298
DB 301 KTKNGLSPIHMAAQGDHLD-CVRLLLQYDAEIDDI-----TLD---HLTPLHVAHCG 349
QY 299 GDKL-KLCMEKTKTDFDTANFANQSPHLHIITOKPDCSVLIDIEFTSRNLDGVLGDDGK 357
DB 350 HHRVAKVLLDKGAKPNSRALN--GFTPLHIAACKNHVRVNMELLLKTGASID--AVTESGL 405
QY 358 NPLHHA--VEHLPPV---ILKGWMDHVKNSEFQDLVNDPDYF-----GNT-IAHYAVKNK 407
DB 406 TPLHVASFMGHLPIVKNLLQRGASPNVSNYK-----VETPLHMAARAGHTEVAKYLLONK 460
QY 408 NADLTFLNMLKASGADLNVRNVGRAPIHVASSNGKANAVSGLVSCGIDVNSQDVNGDTP 467
DB 461 -----AKVNAKAKDDQTPHCAARIGHTNMVKLLLENNANFNLTAGHTP 506
QY 468 LHIAVEGSGMETVLAVLNQRGADVSVQNDGVTPLMSAAKYDGVITKAL--GSAKPNIK 525
DB 507 LHIAAREGHVETVLALL-EKEASQACMTKGGFTPLHVAAYKGVKRVAAELLEDHAPNAA 565
QY 526 GEDTVAKSLMEDYKGTFTPLHFVAGGSGRDTFRVRKNYKCKHDLATIRAAALMQDRSGGE 585
DB 566 GKN-----GLTPLHVAHNNLDIVKL----- 587
QY 586 LVNLGDFESENILGSPNAKFLQIQSANFGFSPARRGIVSSNHNVMKDIILNFVGDLSHL 645
DB 588 LLPRG-----GSP-----HSPAWN-CYTPHIAAKQNVQVEARSLQY-GGSANAE 631
QY 646 SERGYNAMQVAALFGDKEAVMLAKSAPSDLNFKTSATPTPLNLACLRGDNVVRGLVG 705
DB 632 SVQGVTPHLHQAEGHAEWVALL--SKQANGNLGNKSGLTPLHLVAQEGHVPVADVLI- 688
QY 706 QHG--IDINRMGSDKNTVLHYAISKGDSELVQKILAHGTGVNCCNNLQOTPLHVAEG 763
DB 689 KHGMVMDATTRMG---YTPLHVASHYGNIKLVKFLLOHQ-ADVNATKLGYSPLHQAQQ 744

QY 764 GPKIVSSLLKAGAVNVNRLLDNGRSLSSAIVPCKEKGVLGVNKL---LDRGADINLD 820
DB 745 GHTDIVTLLKNGASPNVSSDGTPLAIA-----KELGVISVTDVLKVTDTESFVLVS 799
QY 821 GDHNILPDQ 829
DB 800 DKHRMSPPE 808
RESULT 10
ABM80426
ID ABM80426 standard; protein; 899 AA.
XX AC ABM80426;
XX DT 18-NOV-2004 (first entry)
XX Tumour-associated antigenic target (TAT) polypeptide PRO80961, SEQ:1071.
DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX Tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic.
OS Homo sapiens.
XX WO2004030615-A2.
PN 15-APR-2004.
XX 29-SEP-2003; 2003WO-US028547.
XX 02-OCT-2002; 2002US-0414971P.
PR (GETH) GENENTECH INC.
PA Wu TD, Zhang Z, Zhou Y;
PI WPI; 2004-347921/32.
DR N-PSDB; ACN37888.
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX Claim 12; SEQ ID NO 1071; 7273pp; English.
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX Sequence 899 AA;

Query Match	8.9%; Score 382.5; DB 8; Length 899;
Best Local Similarity	25.8%; Pred. No. 1.7e-20;
Matches 163; Conservative 91; Mismatches 246; Indels 131; Gaps 24;	
QY	209 EILDIIFNSESIA---EGISNPLHADVDNNPVKAGKNVMTLMHLVYACDVPDPRIVKALG 265
Db	33 EVVKLLVSGAEVTCCKKSYTFLHAASSGMSVVKYLL-----72
QY	266 EYVENDEGDIGA-----NAYNVLDSGNLPLHAAKNCTGDKLKLCKEKTCTDIDTANFA 320
Db	73 -----DLGVDNBEFNAY-----GNTPLHVACYN-----GQDVVVNELIDCGAIV 111
QY	321 NQ-----SPLHIITQKPCSVLDEEFTSRNLDGLVDGDKGNPLHHAHVEHLPVLKG 374
Db	112 NQNEKGFTPLHFAAASHTH-GALCILELLVNGADVNMKSKGKTPHMTALH-----G 163
QY	375 VMDHVKNSEFQDLVNDPDYFGNTTAHYAVKKNADLTFLFNMLKASGADLVNRNVGRAP 434
Db	164 RFSRGTIIQSGNAVIDCEDKNGNTPHIAARYGHE--LLINTLITSGADTAKRGHGMFP 221
QY	435 IHVASNGKANAVSGLVSCGIDVNSQDVNGDTPFLHIAVEGSGMETVLAVLNORGADSVSQ 494
Db	222 LHLAALSGFSDCRKLSSGFDIDTDPDFGRTCLHAAAGGNLECLNLLIN-TGADFNKK 280
QY	495 NNDGVTPLMSAAKYGDIGVIKALGSAKPNIKGEDTVAKSLLMEDYKFTPLHVFAGGSR 554
Db	281 DXFGRSPLHYAANCNYQCLFALVSGASVNDLDE-----RGCTPLHYAA---TS 327
QY	555 DTFPRVVRKNYEKCHDLATIRAAALMODRSGGELVNLGDFESNILGSPNAKFLQHIQSANF 614
Db	328 DT-----DQKCLEYLLRNDANFG-----TRDKQGYNAV-----H-YSAAY 361
QY	615 GFSPARGIVSNHNNVMDIL-----NFVGSLSLHLPSERGYNAMQVAALFGDKAVKML 668
Db	362 GHLKCLQLIAS---ETPLDVLMTSGTDMLSDS---DNRATTISPLHLAAHYGHQALEVL 415
QY	669 AKSAPKDLNFKTSATPTPLNLACLRGNEVRGLVGQIGDIINQRMGSDKNTVLHYALS 728
Db	416 VQSL--LDLVDNRSSGRTPLDLAFAFKGHVECDVDLINO-GASTLVKDYILKRTPTHAAT 472
QY	729 KGDSFLVQKILAH---TGVDVNCENNLGOTPLHLAVEGDPKPIVSSLLKAGAVNRLDD 784
Db	473 NGHSECLRLIIGNAEFQNAVDIQDGN--GQTPMLSLVNLGHTDCVYSLLKNGANVDAKD 530
QY	785 NGRSVLSSAIVPGRKEKGVIGVKNLLDRGA 815
Db	531 WGRTHLRGAVTGHEE-----CVDALLQHGA 556
RESULT 11	
ABU11523	
XX	ABU11523 standard; protein; 1536 AA.
XX	ABU11523;
AC	ABU11523;
XX	12-FEB-2003 (first entry)
DT	Human MDDT polypeptide SEQ ID 470.
DE	
KW	MDDT; human; disease detection and treatment molecule polypeptide;
KW	anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW	haemostatic; nephrotropic; antianemic; antipsoriatic; hepatocytic;
KW	gene therapy; protein replacement therapy; cell proliferative disorder;
KW	cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW	anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW	Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW	psoriasis; hepatitis.
OS	Homo sapiens.
XX	WO200279449-A2.
PN	
XX	

PD	10-OCT-2002.
XX	27-MAR-2002; 2002WO-US009944.
XX	28-MAR-2001; 2001US-0279619P.
PR	29-MAR-2001; 2001US-0280067P.
PR	29-MAR-2001; 2001US-0280068P.
PR	16-MAY-2001; 2001US-0291280P.
PR	17-MAY-2001; 2001US-0291829P.
PR	17-MAY-2001; 2001US-0291849P.
PR	19-JUN-2001; 2001US-0299428P.
PR	20-JUN-2001; 2001US-029976P.
PR	20-JUN-2001; 2001US-030001P.
XX	(INCY-) INCYTE GENOMICS INC.
PA	Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
XX	Duffour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI	Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI	Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI	Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX	WPI; 2003-058431/05.
DR	N-PSDB; ABX34513.
XX	New purified disease detection and treatment molecule proteins and
PT	polynucleotides, useful for diagnosing, treating or preventing cancers
PT	(e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT	or hepatitis.
XX	Claim 27; SEQ ID NO 470; 339pp + Sequence Listing; English.
PS	This invention describes a novel disease detection and treatment molecule
CC	polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC	osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC	antianemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC	and the polypeptides of the invention can be used for gene therapy,
CC	protein replacement therapy and are useful for treating a variety of
CC	diseases or conditions. These polypeptides or polynucleotides are
CC	particularly useful for diagnosing, treating or preventing cell
CC	proliferative disorders (e.g. cancers including adenocarcinoma,
CC	leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC	disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC	syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC	hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
CC	by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 1536 AA;
SQ	
Query Match	8.9%; Score 382.5; DB 6; Length 1536;
Best Local Similarity	27.7%; Pred. No. 4e-20;
Matches 156; Conservative 84; Mismatches 206; Indels 117; Gaps 26;	
QY	289 PLHAAKNTGDKL-KLCMEKTKTDFIDTANFANOSPLHIITQKPCSVLDEEFTSRNL 347
Db	68 PLHVA--HGHHRVAKVLLDKGAKPNSRALN--GFTPLHIACKNHRVMEILLTKGASI 124
QY	348 DFLGVGDKGNPLHHA--VEHLPPV---ILKGMVDHKNSSSEFQDLVNDPDYF---GNT 398
Db	125 D--ATESGLTFLHVASFMGHLPIVKNLLQORGASPNVSVK-----VETPLHMAARAGHT 177
QY	399 -IAHYAVKKNADLTFLFNMLKASGADLVNRNVVGRAPIHVASNKNKANAVSGLVSCGIDV 457
Db	178 EVAKYLLQNK-----AKVNAKAKDDQTPHLCAARIGHNTNNVGLLENNANP 223
QY	458 NSQDVNGDTPHIAVEGSGMETVLAVLNORGADVSVQNNDGVTPLMSAAKYGDIGVIKAL 517
Db	224 NLATTAGTFLHIAAREGHVETVLALL--EKEASQACMTKKGFTPLHVAKYGKRVALL 282
QY	518 --GSAKPNIKGEDTVAKSLLMEDYKFTPLHVFAGGSRDTPFRVVRKNYEKCHDLATIRA 575

XX DE Novel human diagnostic protein #7366.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS71562.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 20; SEQ ID NO 37734; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (II) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 4386 AA;
SQ
Query Watch 8.8%; Score 377.5; DB 4; Length 4386;
Best Local Similarity 25.5%; Pred. No. 5e-19;
Matches 175; Conservative 92; Mismatches 277; Indels 141; Gaps 26;
QY 184 TSGPVRADIRIVASKGDLSEDOVEIILIFWNES-----ETAEIGISNPLH----- 230
DB 204 TKGKVLPLALHAARXOD-----TKAALLQNDNADVESKSGFT-PLHIAHYGNIN 256
QY 231 -----ADVNNPVGAKNVMTLMHLVYACDVPRIKALGEVNDGDLGANYNV 281
DB 257 VATLLNRAAAVDFT-----ARNDITPLH-VASKRGNNANVKLL-----LDRGAK-IDA 303
QY 282 LQSEGNLPLHHAARKCTGDKLCKMEKTKTDFIDTANFANQSPHLIITQKPCSVLDIEE 341
DB 304 KTRDGLTPLHCGARSQHEQVEMLLDRAAPILSKTKN--GLSPLHMAWQGDHLNCVOL-- 359
QY 342 FTSRNLDLFGVLDGDKGNPLHHAVERHPLPVILKGMVDHVNKNSSEFQDLVNDPDYFGNTIAH 401

Db 360 LLQHNVPVDDVTNDYLTALHVAACHGKYKAKVLLDKKANP-----NAKALNGFTPLH 412
QY 402 YAVKQKADLTFLFNLKASGADLVNRVNVGRAPTHVASSNGKANAVSGLVSCGIDVNSQD 461
Db 413 IACK-KNR-IKVMELLKKGASIQAVTESGLTPIHVAAPFMGHVNVISQJMEHGHASPNNTN 470
QY 462 VNGDTPLHIAVEGSGMETVLAVLNQRGADVSVQNNQDVTPLMSAAKYGDIGVICAL--GS 519
Db 471 VRGETALHMAARSGQAE-VVRYLVQDGAQVEAKKDDOTPLHISARLGKADIVQOLLQOG 529
QY 520 AKPNI-----KGEDTVA-----KSLLMEDYKGTFTPLHFVAGGSRDTR 558
Db 530 ASPNAATTSGYTPHLHSAREGHEDVAFLDLHGASLSITTKKGTPLHVA----- 580
QY 559 VVRKNYEKCHDLATIRAAALMDRSGGELVNLGDESENIL-----GSPNAKFLQHLQSANF 614
Db 581 -----KYGKLEVANLLLOKSGSPDA-----AKGS 604
QY 615 GFSPARRGIVSSNHNVMKDILNFVGDLSLHLPSERGYNAMQVAALFGDKEAVKMLAKSAP 674
Db 605 GLTPLHVAHYDNQKVALLLLD-QGASPHAAKNGYTPHLHTAAKQNDIATTLLEYG-- 661
QY 675 SDLNFKTSATPTPLNLACLRGDNVVRGLVGOH-GIDINQRMGSKNTVTLHYAISKGSDF 733
Db 662 ADANAVTRQGIASVHLAAQEGHVDVMSLLGRNANVLSNKSGL---TFLHLA-AQEDRV 717
QY 734 LVQKILAHGTVDVNCENNLGOTPLHLAVEGGDPKIVSSLLKAGAVVNRLLDNGRSVLSSA 793
Db 718 NVAEVLVNOGARHVDQAOTKMGYTPHLVHGCHYNIKIIVNELLQHSAKVNAKTKNGYTPHLHOA 777
QY 794 IVPGRKEKGVLGIVNKLDRGADIN 818
Db 778 -----AQGHTHTIINVLLQNNASPN 797
RESULT 14
ADRO8749
ID ADRO8749 standard; protein; 687 AA.
AC ADRO8749;
DT 04-NOV-2004 (first entry)
DE Human protein useful for treating neurological disease Seq 2255.
KW human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW tranquiliser.
OS Homo sapiens.
XX EP1447413-A2.
XX 18-AUG-2004.
PF 12-FEB-2004; 2004EP-00003145.
PR 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX WPI; 2004-583265/57.
XX N-PSDB; ADRO6793.
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

Claim 1; SEQ ID NO 2255; 2686pp; English.

Sequence 687 AA;

Query Match	8.7%	Score 373.5;	DB 8;	Length 687;
Best Local Similarity	24.0%	Pred. No. 5.9e-20;		
Matches 190;	Conservative 115;	Mismatches 299;		
Indels 187;	Gaps 35;			

QY	72	VEDDEDLPPTLPPRTFFSGEGYDDGVSMPTVSRGIYQP-----IVODSNLYSSI-GGVPQ	126
	:	:	:
	:	:	:
Db	9	LEEVEDESPAFISK-----LPQENKSLHSPSGNVLRYPSLVQAIFNGDGD	55

Qy	127	EAQYDAARAGPRKFLYGPYTSNQGIMDFDTPWPDVNRNALGNKEIKE	-----	179
Db	56	EV-----RALIFK-----KEDVNFQDNKRKTPLHAA--AYLGDAEIIELLILSGA	98	

Qy	180	-----EWLTTSGPVRDIADRVASKGDLSEDOVEEILDIIIPNVESEIAGEISN----	PL 229
		:	
Db	99	RVNAKDSKWLTT-----PLH-----RAVASCS-----EAAQVLLKHSADYNARDKNWQPL 144	

Qy	230	HADVDNPNVKGAKNVMTLMHLVYACVDVDPRI	VTKALGEVND	EGDLGANNAYNVLDSEGNLP	289
Db	145	HIAAANKVKGAAALVPLLSNV	-----	NVSDRAGR	176

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Qy      290 LHHAAKNCCTGDKLKLCKEKTCTDFTDTANFANOSPLHIITQKDCPSVLDEETSRNULDF   349
Db      177 LHHAAGSGHGENVMVKKLLSRGAN--INAFKDDRRAIHWAAAYMGHIEYVKLL-LVSHGAEV   232
```

Qy	350	GLV	DG	DN	PL	HH	AV	EH	PP	V	L	K	G	V	M	H	V	K	S	E	F	Q	L	V	N	D	P	P	F	G	N	T	I	A	H	V	A	K	N	K	N	A	409				
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:									
Db	233	T	C	K	D	K	S	Y	T	P	L	A	A	S	-----	S	G	M	T	S	V	K	Y	L	L	D	L	G	L	D	M	N	E	N	A	G	N	T	P	L	H	V	A	C	N	-GQ	284

Qy	468		DLTLFNLKASGADLNVRNVVGRAPIH-VASSNGKANAVSGLYSCGIDVNVSQDVNGDTPL
Db	343		DVVV-NELIDCGAIVNQNEKGFTPLHPAAASTHGALCLELLVNGADVNMESKDGTPL

QY	469	HI	AVEGSGMETVLAVLNQRGADVSVQNNNDGVTPLMSAKYGDTCVILKGSAPNIKED	538
Db	344	HT	ALHGRFSRSQTII-QSGAVIDCEDCKNGNTPLHIAARYGHELLINTLIS----	397

Qy	529	TVAKSLLMEDYKGFPLHFVAGGSRDTRVVRKNYEKCHDLATI----	RAALMQDRSGG	584
	:	:	:	:
	:	:	:	:
Db	398	TAKRGI-----HGMFPLHLAALSGFSD---CCRKLLSSGFDIDTPDDFGRTCLHAAAGG	449	

Qy	640
Db	500

Qy	641	-----SLH-----	-----LPSEGCYNMQVAALFGDKEAVKMLAKS	671
			:	
Db	501	DERGCTPLHYAATSDTGKCLEYLLRNDANPGRVDRKQGYNAVHYSAAVGHLCCLQLIA-S	559	

672	Qy	AKPSDLNFKTS-----APTPFLNIACLRGNEVVRGLVGQHGDIDINORMGSDKN	720
		: : :	
560	Db	ETPLDVLMTSGTDMLSDDNRATISPLHLAAAYGHGHALELV-QSLLDLDVRNSSGR-	617
		: : :	
721	Qy	TVLHVAISKGSFELVKLIHAHTGVNDVCENN-LQPTPLHLAVGGDPKIVSSLLKGAVV	779
		: : :	
618	Db	TPDLDAAFKHVECD-VLINQGASILVKDVIYIKRTPIHAAATNGHSECLRLLIIGNAEPO	676
		: : :	
780	Qy	NRL----DNQR	787
		: : :	
677	Db	NAVDIQDNGO	687

RESULT 15

AAE33684

ID AAE33684 standard; protein; 1056 AA.

AC AAE33684;

DT 16-APR-2003 (first entry)

DE Human structural and cytoskeleton-associated protein (SCAP) #18.

Human; structural and cytoskeleton-associated protein; SCAP; leukaemia; cell proliferative disorder; actinic keratosis; cancer; gastroenteritis; cirrhosis; psoriasis; adenocarcinoma; Kratochvil-Jakob disease; stroke; sarcoma; neurological disorder; epilepsy; seasonal affective disorder; Huntington's disease; Alzheimer's disease; lymphoma; melanoma; myeloma; anxiety; schizophrenia; amnesia; viral infection; pneumonia; influenza; arteriosclerosis; smallpox; Colorado tick fever; rabies; gene therapy; neuroprotective; nootropic; neuroleptic; cytosstatic; virucide.

Homo sapiens.

XX	Key	Location/Qualifiers
FH		

FH	key	localtion/
FT	Binding-site	867: .874

FT /note= "ATP/GP-binding site motif A"

PN WO2002101009-A2.

19-DEC-2002

XX
PF
06-JUN-2002. 2002WO-IIS017956

XX
DE JUN 2001 - 2001118 0206865D

PR 07-JUN-2001; 2001US-0296865P.
 PR 08-JUN-2001; 2001US-0296878P.

PR 08-JUN-2001; 2001US-0296878P.
 PP 15-JUN-2001; 2001US-0298554P.

PR 15-JUN-2001; 2001US-0298664P.
PP 21-JUN-2001; 2001US-0300149P

FR 21-JUN-2001; 2001US-0300149P
PR 29-JUN-2001; 2001US-0302340P

PK 25-JUN-2001; 2001US-0302340F:
PR 06-JUL-2001: 2001US-0303481P:

08-JUL-2001: 2001US-0303481E:
12-JUL-2001: 2001US-0305059P:

21-DEC-2001; 2001US-0343557P.

PA (INCY-) INCYTE GENOMICS INC.

PI Tang TV, Warren BA, Honchell CD, Richardson TW, Elliott VS;
PI Walla NK, Yue H, Batra S, Griffin JA, Baughn MR, Forsythe IJ;
PI Burford N, Emerling BM, Sanjanwala MM, Khan FA, Lu DAM, Hafalia AJA;
PI Nguyen DB, Yang J, Li JX, Becha SD, Yao MG, Gietzen KJ, Luo W;
PI Lee EA, Ison CH, Lasek AKW;

WPB: 2003-148791 /

DR N-PSDB; AAD51581.
XX
PT New human structural and cytoskeleton-associated proteins and genes,
PT useful for diagnosing or treating cancers (e.g. leukemia or lymphoma),
PT viral infections (e.g. influenza) or neurological disorders (e.g.
PT epilepsy or stroke).

XX
PS
Claim 1: Col 195-198: 121pp: English.

xx The invention relates to human structural and cytoskeleton-associated
cc proteins (SCAP) and genes. SCAP sequence and agonist are useful for
cc


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Db 566 GKN-----GLTPLHVAHNNLDIVKL----- 587
QY 586 LVNLGDFESENILGSPNAKFLQHIQSANFGSPARRGIVSSNNHNMKDILNFGVDSLHLP 645
Db 588 LLPRG-----GSP-----HSPAWN-GYTPHLHIAKQNVQVEVARSLQY-GGSANAE 631
QY 646 SERGYNAMOVAALFGDKAEAVKMLAKSPKDLNFKTSATPTPLNLACLRLGDNVEVVRGLVG 705
Db 632 SVQGVTPHLAAQEGHAEMVALL--SKOANGNLGNKSGLTPLHLVAQEGHVPVADVLI- 688
QY 706 QHG--IDINQMGSDKNTVLHYAISKGDSFLVKILAHGTVDVNCENNLGQTPHLHAEVG 763
Db 689 KHGVMVDATTMVG---YTPHLVASHYGNIKLVKFLQHQ-ADVNAKTKLGYSPLHQAQQ 744
QY 764 GPKIVSSLLKAGAVNRLDDNGRSLSSAIVPGRKEKGVIVNKL---LDRGADINLD 820
Db 745 GHTDIVTLLKNGASPNVSSDGTTPLAIA-----KRLGYISVTDVLKVVTDTSFVLVS 799
QY 821 GDHNLFDQ 829
Db 800 DKHRMSFPE 808

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RESULT 6

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US-09-949-016-9010
; Sequence 9010, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9010
; LENGTH: 1883
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9010

```

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Query Match          9.1%; Score 390.5; DB 4; Length 1883;
Best Local Similarity 26.0%; Pred. No. 5.7e-24;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

QY 194 RIVASKGDLSEDOVEEILDIIIFMNESEIAEGISNPLHADVDNPNVK-----GA---- 241
Db 259 RLLLDGGAQIETKTDEL-----TPLHCAARNGHVRISEILLDHGAPIQA 303
QY 242 --KNVMTLHVLVYACD-VDPRIVKALGEVNDGDLGANYVNLSEGNLPLHAAKNT 298
Db 304 KTKNGLSPIHMAAQGDHLD--CVRLLQYDAEIDDI-----TLD---HLTPLHVAHCG 352
QY 299 GDKL-KLCWEKTKTDFIDTANFANQSPHLHITQKPCSVLDIEEFTSRNLDPLGVDGDK 357
Db 353 HHRVAKVLLDKGAKPNSRALN--GFTPLHIAKKNHVRVWELLKTGSID--AVTESGL 408
QY 358 NPLHHA--VEHLPPV---ILKGVMHVKNSSSEFQDLVNDPDYF-----GNT-IAHVAVKK 407
Db 409 TPLHVASFMGHLPIVKNLLQRGASPNVSNVK-----VETPLHMAARAGHTEVAKYLLQNK 463
QY 408 NADTLFLNMLKASGADLNVRNVGRAPIHVASSNGKANAVSGLVSGCIDVNSQVNDGTP 467
Db 464 -----AKNKAADDQTPHLCAARIGHNTNMVKKLLENNANPNLATAGTTP 509
QY 468 LHIAVEGGSNETVLAVLNQRGADVSQVNDGVTPLMSAAKYDGIKAL--GSAKPNIK 525

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Db 510 LHIAAREGHVETVLALL-EKEASQACWTKKGFTPLHVAAYKGVKVAELLERDAHPNAA 568
QY 526 GEDTVAKSLLMEDYKGTPLHVFAGGSRDTRFVVRKNYKCHDLATIRAAALMQDRSGGE 585
Db 569 GKN-----GLTPLHVAHNNLDIVKL----- 590
QY 586 LVNLGDFESENILGSPNAKFLQHIQSANFGSPARRGIVSSNNHNMKDILNFGVDSLHLP 645
Db 591 LLPRG-----GSP-----HSPAWN-GYTPHLHIAKQNVQVEVARSLQY-GGSANAE 634
QY 646 SERGYNAMOVAALFGDKAEAVKMLAKSPKDLNFKTSATPTPLNLACLRLGDNVEVVRGLVG 705
Db 635 SVQGVTPHLAAQEGHAEMVALL--SKOANGNLGNKSGLTPLHLVAQEGHVPVADVLI- 691
QY 706 QHG--IDINQMGSDKNTVLHYAISKGDSFLVKILAHGTVDVNCENNLGQTPHLHAEVG 763
Db 692 KHGVMVDATTMVG---YTPHLVASHYGNIKLVKFLQHQ-ADVNAKTKLGYSPLHQAQQ 747
QY 764 GPKIVSSLLKAGAVNRLDDNGRSLSSAIVPGRKEKGVIVNKL---LDRGADINLD 820
Db 748 GHTDIVTLLKNGASPNVSSDGTTPLAIA-----KRLGYISVTDVLKVVTDTSFVLVS 802
QY 821 GDHNLFDQ 829
Db 803 DKHRMSFPE 811

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RESULT 7

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US-09-949-016-9011
; Sequence 9011, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9011
; LENGTH: 1883
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9011

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Query Match          9.1%; Score 390.5; DB 4; Length 1883;
Best Local Similarity 26.0%; Pred. No. 5.7e-24;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

QY 194 RIVASKGDLSEDOVEEILDIIIFMNESEIAEGISNPLHADVDNPNVK-----GA---- 241
Db 259 RLLLDGGAQIETKTDEL-----TPLHCAARNGHVRISEILLDHGAPIQA 303
QY 242 --KNVMTLHVLVYACD-VDPRIVKALGEVNDGDLGANYVNLSEGNLPLHAAKNT 298
Db 304 KTKNGLSPIHMAAQGDHLD--CVRLLQYDAEIDDI-----TLD---HLTPLHVAHCG 352
QY 299 GDKL-KLCWEKTKTDFIDTANFANQSPHLHITQKPCSVLDIEEFTSRNLDPLGVDGDK 357
Db 353 HHRVAKVLLDKGAKPNSRALN--GFTPLHIAKKNHVRVWELLKTGSID--AVTESGL 408
QY 358 NPLHHA--VEHLPPV---ILKGVMHVKNSSSEFQDLVNDPDYF-----GNT-IAHVAVKK 407
Db 409 TPLHVASFMGHLPIVKNLLQRGASPNVSNVK-----VETPLHMAARAGHTEVAKYLLQNK 463

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Db 304 KTKNGLSPHMAAQGDHLD--CVRLLLQYDAEIDDI-----TLD---HLTFLHVAHAHC 352
Qy 299 GDKL-KLCMEKTKTDFIDTANFANQSPHLIIITQKPCDSCVLDIEEFTSRNLDPLGLVDGDK 357
Db 353 HHRVAKVLLDQKAKPNSRALN--GFTPLHIACKKNHVRVMEILLKTGASID--AVTESGL 408
Qy 358 NPLHHA--VEHLPPV---ILKGVMDHVKNSSFDLVNDPDYF---GNT-IAHYAVNKK 407
Db 409 TPLHVASPMGHLPIVKNLLQRGASPNVSVK-----VETPLHMAARAGHTEVAKYLLQNK 463
Qy 408 NADLTFLFNLKASGADLNVRNVGRAPIHVASSNGKANAVSLGSCGIDVNSQDVNGDTP 467
Db 464 -----AKVNAKAKDDQTPHLCAARIGHTNNMVKLLLENNANPNLATTAGHTP 509
Qy 468 LHIAVEGSGMETVLAVLNORGADVSQNNNDGVTPMLSAKYGDIGVICAL--GSAKPNIK 525
Db 510 LHIAREGHVETVLALL--EKEASQACMTKKGFTPLHVAAYKGVKRVAEILLERDAHPNAA 568
Qy 526 GEDTVAKSLMEDYKGFTHFVAGGSRDTRFVRVKNYKCHDLATIRAAALMQDRSGE 585
Db 569 GKN-----GLTFLHVAHVHNNLDIVKL----- 590
Qy 586 LVNLGDFESENILGSPNAKFLQHOISANFGSPARRGIVSSNNHVMKDIILNFVGDLSHLP 645
Db 591 LLPRG-----GSP-----HSPAWN-GYTPLHIAAKQNVARSLLQY--GGSANAE 634
Qy 646 SERGVNAMOVALFGDKEAVKMLAKSAKPSDLNFKTSATPTPLNACLARGDNEVVRGLVG 705
Db 635 SVQGVTPHLAAQEGHAEVALLL--SKOANGNLGNKSLGTLPLHLVAQEGHVPVADVLI- 691
Qy 706 QHG--IDINQMGSDKNVTLVHVAISKGDSFLVKILAHGTGVVNCENNLGOTPLHLAVEG 763
Db 692 KHGVWVDATIRMG---YTPPLHVAHYGNIKLVKFLQHQ--ADVNAKTKLGYSPHLQAAQ 747
Qy 764 GPKIVSSLLKAGAVNRLDDNGRSVLSSAIVPGRKEKGVIGVKNL---LDRGADINLD 820
Db 748 GHTDIVTLLKNGASPNESVSDGTTPLAIA-----KRLGYISVTDVLKVVTDTSFVLVS 802
Qy 821 GDHNLFDQ 829
Db 803 DKHRMSFPE 811

RESULT 10

US-09-949-016-9014
; Sequence 9014, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9014
; LENGTH: 1883
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9014

Query Match 9.1%; Score 390.5; DB 4; Length 1883;

Best Local Similarity 26.0%; Pred. No. 5.7e-24;

Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

Qy 194 RIVASKGDLSEQVEILDIIIFWNESEIAEGISNPLHADVDNPNVK-----GA---- 241

Db 259 RLLDRGAQIETTKKDEL-----TFLHCAARNGHVRISSEILLDHGAPIQA 303
Qy 242 --KNVMTIMLVUYACD--VDPPIVAKALGEVNDGDLGANAYVLDSEGNLPLHHAKNCT 298
Db 304 KTKNGLSPHMAAQGDHLD--CVRLLLQYDAEIDDI-----TLD---HLTFLHVAHAHC 352
Qy 299 GDKL-KLCMEKTKTDFIDTANFANQSPHLIIITQKPCDSCVLDIEEFTSRNLDPLGLVDGDK 357
Db 353 HHRVAKVLLDQKAKPNSRALN--GFTPLHIACKKNHVRVMEILLKTGASID--AVTESGL 408
Qy 358 NPLHHA--VEHLPPV---ILKGVMDHVKNSSFDLVNDPDYF---GNT-IAHYAVNKK 407
Db 409 TPLHVASPMGHLPIVKNLLQRGASPNVSVK-----VETPLHMAARAGHTEVAKYLLQNK 463
Qy 408 NADLTFLFNLKASGADLNVRNVGRAPIHVASSNGKANAVSLGSCGIDVNSQDVNGDTP 467
Db 464 -----AKVNAKAKDDQTPHLCAARIGHTNNMVKLLLENNANPNLATTAGHTP 509
Qy 468 LHIAVEGSGMETVLAVLNORGADVSQNNNDGVTPMLSAKYGDIGVICAL--GSAKPNIK 525
Db 510 LHIAREGHVETVLALL--EKEASQACMTKKGFTPLHVAAYKGVKRVAEILLERDAHPNAA 568
Qy 526 GEDTVAKSLMEDYKGFTHFVAGGSRDTRFVRVKNYKCHDLATIRAAALMQDRSGE 585
Db 569 GKN-----GLTFLHVAHVHNNLDIVKL----- 590
Qy 586 LVNLGDFESENILGSPNAKFLQHOISANFGSPARRGIVSSNNHVMKDIILNFVGDLSHLP 645
Db 591 LLPRG-----GSP-----HSPAWN-GYTPLHIAAKQNVARSLLQY--GGSANAE 634
Qy 646 SERGVNAMOVALFGDKEAVKMLAKSAKPSDLNFKTSATPTPLNACLARGDNEVVRGLVG 705
Db 635 SVQGVTPHLAAQEGHAEVALLL--SKOANGNLGNKSLGTLPLHLVAQEGHVPVADVLI- 691
Qy 706 QHG--IDINQMGSDKNVTLVHVAISKGDSFLVKILAHGTGVVNCENNLGOTPLHLAVEG 763
Db 692 KHGVWVDATIRMG---YTPPLHVAHYGNIKLVKFLQHQ--ADVNAKTKLGYSPHLQAAQ 747
Qy 764 GPKIVSSLLKAGAVNRLDDNGRSVLSSAIVPGRKEKGVIGVKNL---LDRGADINLD 820
Db 748 GHTDIVTLLKNGASPNESVSDGTTPLAIA-----KRLGYISVTDVLKVVTDTSFVLVS 802
Qy 821 GDHNLFDQ 829
Db 803 DKHRMSFPE 811

RESULT 11

US-09-949-016-9015
; Sequence 9015, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9015
; LENGTH: 1883
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9015


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Query Match          9.1%; Score 390.5; DB 4; Length 1883;
Best Local Similarity 26.0%; Pred. No. 5.7e-24;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

QY 194 RIVASKGDLSEDOVEEILDIIFMNESEIAEGISNPLHADVDNPNVK-----GA----- 241
DB 259 RLLDRGAQETETKDEL-----TPLHCAARNGHVRISSEILLDHGAPIQA 303
QY 242 --KNVMTLMLHVACD--VDPRIKALGEVENDGDLGANAYVNLDSGNLPLHAAKNCT 298
DB 304 KTKNGLSPIHMAAGDHL--CVRLLOYDAEIDDI-----TLD---HLTPLHVAACG 352
QY 299 GDKL-KLCMEKTKTDFIDTANFANQSPHLHIITQKPCSVLIDIEFTSRNLDGVLGDGK 357
DB 353 HHRVAKVLLDKGAKPNSRALN--GFTPLHIACKKNHVRVMEILLKTGASID--AVTESGL 408
QY 358 NPLHHA--VEHLPPV---ILKGWMDHVKNSEFQDLVNDPDPF-----GNT-IAHYAVKN 407
DB 409 TPLHVASFMGHLPVKNLLQRGASPNVNVK-----VETPLHMAARAGHTEVAKYLLONK 463
QY 408 NADLTFLNMLKASGADLNVRNVGRAPIHVASSNGKANAVSGLVSCGIDVNSQDVNGDTP 467
DB 464 -----AKVNAKAKDDQTPHCAARIGHTNMVKLLLENNANFNLTATTAGTTP 509
QY 468 LHIAVEGSGMETVLAVLNQAGADVSVQNNQDVTPLMSAAKYDGIKAL--GSAKPNIK 525
DB 510 LHIAAREGHVETVLALL--EKEASQACMTKKGFTPLHVAAYKGVKRVVAELLLERDAHPNAA 568
QY 526 GEDTVAKSLLMEDYKGTFTPLHFVAGGSRDTPFRVVRKNYEKCHDLATIRALMQDRSGGE 585
DB 569 GKN-----GLTPLHVAHVHNNLDIVKL----- 590
QY 586 LVNLGDPFESENILGSPNAKFLQHQSANFGFSPARRGIVSSNNHNMKDIILNFVGDLSLHLP 645
DB 591 LLEPRG-----GSP-----HSPAWN-GYTPHIAAKQNVQVEVARSLLOY--GGSANAE 634
QY 646 SERGYNAMQVAALFGDKAEVKMLAKSAKPSDLNFKTSATPTPLNLACLGRDNEVVRGLVG 705
DB 635 SVQGVTPHLHAAQEGHAEMVALL--SKQANGNLGNKSGLTPLHLVAQEGHVPVADVLI- 691
QY 706 QHG--IDINQRMGSKNTVLHVAISKGDSFLVQKILAHGTGVNVCNNLQOTPLHLAVEG 763
DB 692 KHGVMVDATTMKG---YTPHVAHYGNIKLVKFLLOHQ--ADVNAKTGLGYSPLHQAAQ 747
QY 764 GDPKIVSSLLKAGAVNRLDNGRSVLSAIVPGRKEKGLVGVNKL---LDRGADINLD 820
DB 748 GHTDITVLLKNGASPNVSSDGTTPLAIA-----KRLGYISVTDVLKVVTDTSFVLVS 802
QY 821 GDHNLFDQ 829
DB 803 DKHRMSFPE 811

RESULT 12
US-09-949-016-9016
; Sequence 9016, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9016
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; LENGTH: 1883
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9016

Query Match          9.1%; Score 390.5; DB 4; Length 1883;
Best Local Similarity 26.0%; Pred. No. 5.7e-24;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

QY 194 RIVASKGDLSEDOVEEILDIIFMNESEIAEGISNPLHADVDNPNVK-----GA----- 241
DB 259 RLLDRGAQETETKDEL-----TPLHCAARNGHVRISSEILLDHGAPIQA 303
QY 242 --KNVMTLMLHVACD--VDPRIKALGEVENDGDLGANAYVNLDSGNLPLHAAKNCT 298
DB 304 KTKNGLSPIHMAAGDHL--CVRLLOYDAEIDDI-----TLD---HLTPLHVAACG 352
QY 299 GDKL-KLCMEKTKTDFIDTANFANQSPHLHIITQKPCSVLIDIEFTSRNLDGVLGDGK 357
DB 353 HHRVAKVLLDKGAKPNSRALN--GFTPLHIACKKNHVRVMEILLKTGASID--AVTESGL 408
QY 358 NPLHHA--VEHLPPV---ILKGWMDHVKNSEFQDLVNDPDPF-----GNT-IAHYAVKN 407
DB 409 TPLHVASFMGHLPVKNLLQRGASPNVNVK-----VETPLHMAARAGHTEVAKYLLONK 463
QY 408 NADLTFLNMLKASGADLNVRNVGRAPIHVASSNGKANAVSGLVSCGIDVNSQDVNGDTP 467
DB 464 -----AKVNAKAKDDQTPHCAARIGHTNMVKLLLENNANFNLTATTAGTTP 509
QY 468 LHIAVEGSGMETVLAVLNQAGADVSVQNNQDVTPLMSAAKYDGIKAL--GSAKPNIK 525
DB 510 LHIAAREGHVETVLALL--EKEASQACMTKKGFTPLHVAAYKGVKRVVAELLLERDAHPNAA 568
QY 526 GEDTVAKSLLMEDYKGTFTPLHFVAGGSRDTPFRVVRKNYEKCHDLATIRALMQDRSGGE 585
DB 569 GKN-----GLTPLHVAHVHNNLDIVKL----- 590
QY 586 LVNLGDPFESENILGSPNAKFLQHQSANFGFSPARRGIVSSNNHNMKDIILNFVGDLSLHLP 645
DB 591 LLEPRG-----GSP-----HSPAWN-GYTPHIAAKQNVQVEVARSLLOY--GGSANAE 634
QY 646 SERGYNAMQVAALFGDKAEVKMLAKSAKPSDLNFKTSATPTPLNLACLGRDNEVVRGLVG 705
DB 635 SVQGVTPHLHAAQEGHAEMVALL--SKQANGNLGNKSGLTPLHLVAQEGHVPVADVLI- 691
QY 706 QHG--IDINQRMGSKNTVLHVAISKGDSFLVQKILAHGTGVNVCNNLQOTPLHLAVEG 763
DB 692 KHGVMVDATTMKG---YTPHVAHYGNIKLVKFLLOHQ--ADVNAKTGLGYSPLHQAAQ 747
QY 764 GDPKIVSSLLKAGAVNRLDNGRSVLSAIVPGRKEKGLVGVNKL---LDRGADINLD 820
DB 748 GHTDITVLLKNGASPNVSSDGTTPLAIA-----KRLGYISVTDVLKVVTDTSFVLVS 802
QY 821 GDHNLFDQ 829
DB 803 DKHRMSFPE 811

RESULT 13
US-09-949-016-9017
; Sequence 9017, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9017
; LENGTH: 1883
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9017

Query Match 9.1%; Score 390.5; DB 4; Length 1883;
Best Local Similarity 26.0%; Pred. No. 5.7e-24;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;
QY 194 RIVASKGDLSEDOVEEILDIIFNNESEIAEGISNPLHADVDPNVK-----CA----- 241
DB 259 RLLDRGAQIETKDEL-----TFLHCAARNGHVRISBILLDHGAPIQA 303
QY 242 --KNVMTLHVLVYACD--VDPRIKALGEVENDEGLGANAYNVLDSEGNLPLHAAKNT 298
DB 304 KTKNGLSPIHMAAQGDHLD--CVRLQLQYDAEIDDI-----TLD---HLTPLHVAACG 352
QY 299 GDKL-KLCMEKTKTDFIDTANFANQSPHLHIITQKPDSCVLDIEEFTSRNLDFGLVDGDK 357
DB 353 HHRVAKVLLDKGAKPNSRALN--GFTPLHIAKKNHVRVMEILLKTGASID--AVTESGL 408
QY 358 NPLHHA--VEHLPPV---ILKGMVHVKNSSFEQDLVNDPDYF-----GNT--IAHYAVKVK 407
DB 409 TPLHVASFMGHLPIVKNLLQRGASPNVNVK-----VETPLHMAARAGHTEVAKYLLQNK 463
QY 408 NADLTFLNMLKASGADLNVRNIVGAPIHVASSNGKANAVSGLVSGIDVNSQDVNGDTP 467
DB 464 -----AKVNAKAKDDQTPHCAARIQHTNMVKKLLENANPNLATAGHTP 509
QY 468 LHIAVEGSMETVLAVLNQRGADVSVQNNNDGVTPLMLSAAYGDI GVIKAL--GSAKPNIK 525
DB 510 LHIAAREGHVETVLALL-EKEASQACWTKKGFTPLHVAAYKGVKRVVAELLERDAHPNAA 568
QY 526 GEDTVAKSLLMEDYKGTPLHVFVAGGSRDTRFVRVKNYEKCHDLATIRAALMQDRSGGE 585
DB 569 GKN-----GLTFLHVAHVHNNLDIVKL----- 590
QY 586 LVNLDGFESENILGSPNAKFLQHIQSANFGFSPARRGIVSSNNHNVKMDILNFGVDSLHP 645
DB 591 LIPRG-----GSP-----HSPAWN--GYTPHLHAAQONQVEVARSLLQY--GGSANAE 634
QY 646 SERGYNAQVAALFGDKAEVKMLAKSAPSDLNFKTSATPTPLNLACLRGDNEVVRGLVG 705
DB 635 SVQGVTPHLAAQEGHAEMVALLL--SKQANGNLGNKSLGTLPLHVAQEGHVPVADVLI- 691
QY 706 QHG--IDINQRMGSDKNTVLHVAISKGDSFLVQKILAHGVDVNCENNLGQTPHLHVEG 763
DB 692 KHGVMVDATRMG---YTPHLVASHYGNLKVFLQHQ--ADVNAKTKLGYSPLHQAQQ 747
QY 764 GPKIVSSLLKAGAVNRLDDNGRSVLSAIVPGRKEKVLGVNKL---LDRGADINLD 820
DB 748 GHTDITVILLKNGASNEVSSDGTTPLAIA-----KRLGIYSTVDVLKVVTDSETSFVLVS 802
QY 821 GDNHILFDQ 829
DB 803 DKHRMSFPE 811

RESULT 14
US-09-949-016-6978
; Sequence 6978, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6978
; LENGTH: 4377
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6978

Query Match 8.8%; Score 377.5; DB 4; Length 4377;
Best Local Similarity 25.5%; Pred. No. 3e-22;
Matches 175; Conservative 92; Mismatches 277; Indels 141; Gaps 26;
QY 184 TSGPVRDIADRIKASGDLSEDOVEEILDIIFNMES-----EIAEGISNPLH----- 230
DB 197 TKGKVRPLPALHIAARKDD-----TKAALLQNDNNADVESKSGFT-PLHIAHYGNIN 249
QY 231 -----ADVNNPVKAKNVMTLHVLVYACDVPRIKALGEVENDEGLGANAYNV 281
DB 250 VATLLNPAADVDT-----AENDITPLH-VASKRGNANMVKLL-----LDRGAK-IDA 296
QY 282 LDSEGNLPLHAAKNTGDKLKCMEKTKTDFIDTANFANQSPHLHIITQKPDSCVLDIEE 341
DB 297 KTRDGLTPLHCGARSGHEQVVEMLLDRAPATLSKTKN--GLSPLHMAQGDHLNVCVL-- 352
QY 342 FTSRNLDFGLVDGKKNPLHHAHVEHLPPVILKGMVHVKNSSFEQDLVNDPDYFNTIAH 401
DB 353 LLQHNVPVDDVTNDYLTALHVAHCHGYKVAKVLDDKANP-----NAKALNGFTPLH 405
QY 402 YAVKNKNAADLTFLNMLKASGADLNVRNIVGAPIHVASSNGKANAVSGLVSGIDVNSQD 461
DB 406 IACK-KNR-IKVMELLKHGASIQAVTESGLTPIHVAAFMGHVNIVSQLMHGASPNITT 463
QY 462 VNGDTPHLHIAVEGSMETVLAVLNQRGADVSVQNNNDGVTPLMLSAAYGDI GVIKAL--GS 519
DB 464 VRGETALHMAARSGQAE--VRYLVQDGAQVEAKAKDDQTPHLHISARLKGADIVQOLLOQ 522
QY 520 AKPNI-----KGEDTVA-----KSLMEDYKGTPLHVFVAGGSRDTRF 558
DB 523 ASPNAATSGVTPLHLSAREGHEDVAAFLPDHNGASLSITTKKGFTPLHVA- 573
QY 559 VVRKNYKCHDLATIRAALMQDRSGELVNLGDFESENIL----GSPNAKFLQHIQSANF 614
DB 574 -----KYGKLEVANLLQKSASPDA-----AGKS 597
QY 615 GFSPARRGIVSSNNHNVKMDILNFGVDSLHLPSEKRGYNAMQVAALFGDKAEVKMLAKSAP 674
DB 598 GLTPLHVAHYADNQKVALLLLD-QGASPHAAAKNGYTPHLHIAAKKNQMDIATLLLEYG-- 654
QY 675 SDLAKEKTSATPTPLNLACLRGDNEVVRGLVQHQ--CIDINQRMGSDKNTVLHVAISKGDSF 733
DB 655 ADANAVTRQGIASVHLAAQEGHVDNMVSLLLGRNANVNLSNKSGL---TPLHLIA-AQEDRV 710
QY 734 LVQKILAHGVDVNCENNLGQTPHLHAVEGGDPKPIVSSLLKAGAVNRLDDNGRSVLSA 793
DB 711 NVAEVLVNGQAHVDAQTQWGYTPHLHVGHYGNIKIVNLFLLQHSKAVNAKTKNGYTPHLQA 770
QY 794 IVPGRKEKVLGVNKLDDRGADIN 818
DB 771 -----AQQGHTHIINVLQNNASPN 790

RESULT 15
US-10-164-595-38
; Sequence 38, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:

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Db 121 IGVVQEAQYDAAARAGGRKFLGYPTFSNGQEIWDFPDVFNVAVLGNKEIKEE 180
Qy 181 WLTTSQPVRIADRIIVASKGLDSEDOVEBILDIIFWNESEIAEGISNPLHADVDNPNVK 240
Db 181 WLTTSQPVRIADRIIVASKGLDSEDOVEBILDIIFWNESEIAEGISNPLHADVDNPNVK 240
Qy 241 AKNVMTLMLHVACDVPRIKALGEVNDGDLGANAENVLDSEGNLPLHHAANKCTGD 300
Db 241 AKNVMTLMLHVACDVPRIKALGEVNDGDLGANAENVLDSEGNLPLHHAANKCTGD 300
Qy 301 KLKLCWEKTKTDFIDTANFANQSPHLIIITQKPDSCVLDIEEFTSRNLDPLGLVDGDKNPL 360
Db 301 KLKLCWEKTKTDFIDTANFANQSPHLIIITQKPDSCVLDIEEFTSRNLDPLGLVDGDKNPL 360
Qy 361 HHAVEHLPPVILKGVMDHVKNSEFQDLVNDPDYFGNTIAHYAVKKNADLTLFNNLKAS 420
Db 361 HHAVEHLPPVILKGVMDHVKNSEFQDLVNDPDYFGNTIAHYAVKKNADLTLFNNLKAS 420
Qy 421 GADLVNRVVRGAPTHVASSNGKANAVSLVSCGIDVNSQDVNGDTPLHIAVEGSMETV 480
Db 421 GADLVNRVVRGAPTHVASSNGKANAVSLVSCGIDVNSQDVNGDTPLHIAVEGSMETV 480
Qy 481 LAVLNQAGADVSVQNDGVTPLMSAAKYDGVKALGSAKPNIKGEDTVAKSLLMEDYK 540
Db 481 LAVLNQAGADVSVQNDGVTPLMSAAKYDGVKALGSAKPNIKGEDTVAKSLLMEDYK 540
Qy 541 GFTPLHFVAGGSRDTRFVRVKNYKCHDLATIRAAALMDRSGGBLVNLDGPFESNIIIGS 600
Db 541 GFTPLHFVAGGSRDTRFVRVKNYKCHDLATIRAAALMDRSGGBLVNLDGPFESNIIIGS 600
Qy 601 PNAKFLQHSQANFGSPARRGIVSSNNHVMKDILNFVGDLSLHLPSERGYNAMQVAALFG 660
Db 601 PNAKFLQHSQANFGSPARRGIVSSNNHVMKDILNFVGDLSLHLPSERGYNAMQVAALFG 660
Qy 661 DKEAVKMLAKSAKPSDLNFKTSATPTPLNLACLRGDNVVRGLVQGHGIDINQRMGSDKN 720
Db 661 DKEAVKMLAKSAKPSDLNFKTSATPTPLNLACLRGDNVVRGLVQGHGIDINQRMGSDKN 720
Qy 721 TVLHYAISKGSFLVQKILAHGTGVNVCENNIGQTPPLHLAVAGGDPKIVSSLLKAGAVN 780
Db 721 TVLHYAISKGSFLVQKILAHGTGVNVCENNIGQTPPLHLAVAGGDPKIVSSLLKAGAVN 780
Qy 781 RLDDNGRSVLSSAIVPGRKEKGVIGLVNKLDRGADINLDGHNILFDQCL 831
Db 781 RLDDNGRSVLSSAIVPGRKEKGVIGLVNKLDRGADINLDGHNILFDQCL 831

RESULT 2

US-10-701-038-1
; Sequence 1, Application US/10701038
; Publication No. US20040121433A1
; GENERAL INFORMATION:
; APPLICANT: McBride, Jere W.
; APPLICANT: Walker, David H.
; TITLE OF INVENTION: P153 and P156 Antigens for the Immunodiagnosis of
; Canine and Human Ehrlichiosis and Uses Thereof
; FILE REFERENCE: D6481
; CURRENT APPLICATION NUMBER: US/10/701,038
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/423,573
; PRIOR FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 831
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: immunoreactive surface protein p153
US-10-701-038-1

Query Match 30.2%; Score 1300.5; DB 16; Length 831;
Best Local Similarity 35.7%; Pred. No. 1e-83;

Matches 297; Conservative 156; Mismatches 265; Indels 113; Gaps 16;
Qy 39 APSEDIYTVIIPKCKETA-APILERSKPTPEPKVEDEDLPPTLPRPTFSGE----- 90
Db 11 AVSEDPYAVPLPKGQRPAPTQVLEE-----DPSVEEEETIAPPLPRNNVGEVEPQBDP 65
Qy 91 -----GY-----DDVGVSMTVS-----GIYQPIVQDS-----NLV-----SSIGVP 125
Db 66 IYQGIQPHOEMEEDPYASLDQVSGAGADGIQENPVQEAAGELEEDIYQDPADPQGLG 125
Qy 126 QEA-QYDAAARAG---GPRKFLYGPYTFNSQEIIMDFDTPPDVNRNAVIGNKEIKEW 181
Db 126 QGGQQLDAQYQGPSIGDQRLVNGPYGNDGSAYMEFD-DVMWEGVRDAVIDHEIDPKF 184
Qy 182 LTTSGPVRDIADRIIVASKGLDSEDOVEBILDIIFWNESEIAEGISNPLHADVDNPNVK 241
Db 185 LVTDLGMRHICDKIVQSEGNLPEPDLBEIIVSLKNDXEGISELINPEYQVDIPNPNVREG 244
Qy 242 KNVMTLMLHVACDVPRIKALGEVNDGDLGANAENVLDSEGNLPLHHAANKCTGD 301
Db 245 RNVMTLHLAYAVNDPRIINAISEVNSFGESLGDGYNIOQADGNLPLHHAANKCNQV 304
Qy 302 LKLCWEKTKTDFIDTANFANQSPHLIIITQKPDSCVLDIEEFTSRNLDPLGLVD-GDGKNPL 360
Db 305 LDNCISKTNSNIINIRFGNQSPHLVMVQNPCCSIGNIQVANECMDPNLIDHPTGRMPI 364
Qy 361 HHAVEHLPPVILKGVMDHVKNSEFQDLVNDPDYFGNTIAHYAVKKNADLTLFNNLKAS 420
Db 365 HYAAE-----AASSE-----VLSYVIRNTKAE----- 386
Qy 421 GADLVNRVVRGAPTHVASSNGKANAVSLVSCGIDVNSQDVNGDTPLHIAVEGSMETV 480
Db 387 -----SPQASA-----VNTQDVNGRTPFLCAAISGNSKGL 416
Qy 481 LAVLNQAGADVSVQNDGVTPLMSAAKYDGVKALGSAKPNIKGEDTVAKSLLMEDYK 540
Db 417 SVMLLQNGVDCAVRDKNYSTPLHYAVAGNDIKSIKNLCSVKGRVQGVKSSAASLLCEDLQ 476
Qy 541 GFTPLHFVAGGSRDTRFVRVKNYKCHDLATIRAAALMDRSGGBLVNLDGPFESNIIIGS 600
Db 477 GDTPLHTACKVEGTAKFETVRQSIKGGHKGQVLQELLIREGSGPRL-NVSGFGSQSILSG 535
Qy 601 PNAKFLQHSQANFGSPARRGIVSSNNHVMKDILNFVGDLSLHLPSERGYNAMQVAALFG 660
Db 536 VSGDLYGLVNSQNPSTSPVHAAVKANNIQLNLNLFKKSFDILROSSPNFVPMHAALFA 595
Qy 661 DKEAVKMLAKSAKPSDLNFKTSATPTPLNLACLRGDNVVRGLVQGHGIDINQRMGSDKN 720
Db 596 DVKTVKLIENASGEVNAQSDSTLTPHLACIRGDSIIKRMVHEHESVNVNQTWGPQN 655
Qy 721 TVLHYAISKGSFLVQKILAHGTGVNVCENNIGQTPPLHLAVAGGDPKIVSSLLKAGAVN 780
Db 656 TVQYAINRGNHSLIKRLLSHPSDLNVRNADGKTSASAMEKGDGLTKVTKALCNAGAVN 715
Qy 781 RLDDNGRSVLSSAIVPGRKEKGVIGLVNKLDRGADINLDGHNILFDQCL 831
Db 716 TVDNGRSVLSSAIVSQNEKLVFIVKLLNSGAKIGSQEDKXNLLQKCI 766

RESULT 3

US-10-291-172-343
; Sequence 343, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19

Db 570 V-QSLDLVRSSGRTPLDLAFAKGVCEVDVNLQGNASILVVDYILKRTPIHAAATNG 628
QY 731 DSEFLVQKILAH-----TGVDVNCNNLQGPPLHLAVEGGDPKTVSILLKAGAVNRLDNG 786
Db 629 HSECLRLLIAGNAEPQNAVDIQGN--GQPLMLSVLNGHTDCVYSILLNKGANVDKRWG 686
QY 787 RSVLSAIVPGRKEKGVGLVKNLLDRGA 815
Db 687 RTALHRGAVTGHEE-----CVDALLQHGA 710

RESULT 5

US-10-479-764-18
; Sequence 18, Application US/10479764
; Publication No. US20050027103A1
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. Tom; WARREN, Bridget A.;
; APPLICANT: HONCHELL, Cynthia D.; RICHARDSON, Thomas W.;
; APPLICANT: ELLIOTT, Vicki S.; CHAWLA, Narinder K.;
; APPLICANT: YUE, Henry; BATRA, Sajeev;
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.;
; APPLICANT: EMMERLING, Brooke M.; SANJANWALA, Madhusudan M.;
; APPLICANT: KHAN, Farrah A.; LU, Dying Aina M.;
; APPLICANT: HAFALIA, April J.A.; NGUYEN, Daniel B.;
; APPLICANT: YANG, Junming; LI, Joana X.;
; APPLICANT: BECHA, Shanya D.; YAO, Monique G.;
; APPLICANT: GIETZEN, Kimberly J.; LUO, Wen;
; APPLICANT: LEE, Ernestine A.; ISON, Craig H.;
; APPLICANT: LASEK, Amy W.
; TITLE OF INVENTION: STRUCTURAL AND CYTOSKELETON-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1007 USN
; CURRENT APPLICATION NUMBER: US/10/479,764
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/US02/17956
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/296,865
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/296,878
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/298,664
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/300,149
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/302,340
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/303,481
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/305,059
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/343,557
; PRIOR FILING DATE: 2001-12-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 489786CD1
US-10-479-764-18

Query Match 8.7%; Score 373.5; DB 17; Length 1056;
Best Local Similarity 23.9%; Pred. No. 1.7e-17;
Matches 198; Conservative 101; Mismatches 303; Indels 227; Gaps 35;
QY 108 OPPIVDSNLSIGVGPQEAQDAARAGGRKFLYGPYTSNGQEIWDFFDTPWPDV 167
Db 9 QPPLVQ-----AIFSGDPPEI-----RMLIHK-----TEDVNTLDSKRTPLHVA 48
QY 168 RNVLNKGKE-----EWLTSGPVRDIADRIVASKGDLSEQVVEILDI 213

Db 49 --AFLGDAEIIIEILLISGARVNAKDNWLT---PLH---RAVASRS-----EEAQVQ 92
QY 214 IFMNESEIAEGISN---PLHADVDNNPKGAKNVTMLMHLVYACDVPRIV---KAL-GE 266
Db 93 LIKESADVNRDKWQTPLVHAAAANKAVKCAEVIIPLSSVNVSDRGRTALHHAALNGH 152
QY 267 VE-----NDEGDLGANAY-----NVLDSGNLPLHH 292
Db 153 VEMVNLILAKGANINAFDKDRRALHWAAYMGHLDVVALLINHGAEVTCCKDKKGYTPUHA 212
QY 293 AAKNCTGDKLK-----LC---MEKTKTDFIDTANFANQ----- 322
Db 213 AASNGQINVVKHLNLGVEIDEINVYNTALHIAICYNQDADVNNELIDYGANVQPNNG 272
QY 323 -SPLHIITQKPDSCVLDIEFTSRNLDPLGLVDGQKQPLHHAHVEHPLPVILKGMWDH--- 378
Db 273 FTPLHFAAASHTH-GALCIELELVNNGADVNIQSKDGKSPHMTAVH-----GRFTRSQ 324
QY 379 -VKSSSEFQDLVNDPDYFGNTIAHVAVKKNADLTLENMLKASGADLNVNVVGRAPTHV 437
Db 325 LIQNGGEIDCVDKD-----GNTPLHVAARYGHE--LLINTLITSGADTAKCGIHSWFPULH 378
QY 438 ASSNGKANAVSGLVSCGIDVNSQDVNGDTPPLHIAVEGGSMETVLAVLNQRGADYSVQND 497
Db 379 AALNAHSDCCRKLSSGFEIDTPDKFGTCLHAAAAGNVESI-KLLOSSGADFHKKDKC 437
QY 498 GVTPLMSAAYGDIQVITKALGSAPNKGEDTVAKSLMEDYKGFPTPLHVFAG----- 550
Db 438 GRTPLHVAANAACHFHCITETLVTTGANVNETD-----DW-GRTALHYAAASDMDRNK 487
QY 551 ---GSRDTPFRVKNYKCHDLATIRAAAL-----MQDRSGGELVN---LG 590
Db 488 TILGNAHDN-----SEELERARELKEKEATLCLEFLQNDANPSIRDKEGYNSIHAAAYG 543
QY 591 DPESNIILGSPNAKFLQHQISANFGFSPARRGIVSSNNHNVMKDILNFVGDLSIHLPSERGY 650
Db 544 HRQCLELL-----LERTNSGFESDSGATKS-----PLHL----- 573
QY 651 NAMQVAALFGDKEAVKMLAKSAKPSDLNFKTSATPTPLNLACLGRDNEVVRLGVQHGID 710
Db 574 ---AAYNGHHQALEVLLQSL--VDLIRDEKGRALTDLAFAKGTCEVREALINQ-GAS 625
QY 711 INQRMGSDQNTVLHVAISKDGSFLVQKIL--AHTGVDVNCNNLQGPPLHLAVEGGDPKI 768
Db 626 IFVQNDVTKRTPHLSASVINGHTLCLRLLELEADNPEAVDVKAGQTPMLAVAYGHIDA 685
QY 769 VSSLLKAGAVVNRLLDDNGRSVLSAIVPGRKEKGVGLVGNKLLDRGADI 817
Db 686 VSLLEKEANVDVTVDILGCTALHRGIMTGHEE-----CVQMLLEQVEI 729

RESULT 6

US-10-108-260A-3237
; Sequence 3237, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3237
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3237

Query Match 8.5%; Score 368.5; DB 15; Length 1330;
Best Local Similarity 25.1%; Pred. No. 5.5e-17;
Matches 178; Conservative 87; Mismatches 262; Indels 183; Gaps 26;

[illegible]

RESULT 7

```

US-10-369-978-4
; Sequence 4, Application US/10369978
; Publication No. US20030152991A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Walker, Richard G.
; APPLICANT: Willingham, Aaron
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A Eukaryotic Mechanosensory Transduction Channel
; FILE REFERENCE: 02307E-097600US
; CURRENT APPLICATION NUMBER: US/10/369, 978
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US/09/392, 812A
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1619
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: amino acid sequence derived from nompC CDNA

```

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; OTHER INFORMATION: sequence
US-10-369-978-4

Query Match      8.5%; Score 368; DB 14; Length 1619;
Best Local Similarity 21.9%; Pred. No. 7.9e-17;
Matches 187; Conservative 133; Mismatches 299; Indels 236; Gaps 35;

Qy   119 SSIQGVPOEA-----QYDAARAGGPKRFLYPPTFSNG-QIIMDFPDTPWP----- 165
Db   22 SSLTGPDESATPSERATPAKADSDPK----DDSSSGDKKKMDL-FPAPKPSPSAGASI 76

Qy   166 -DVNNAVLGNKBIKEEMLTTSGPVRIADRIVASKGLDSEDOVEBIIIDLIIFMNESEIAEG 224
Db   77 RDTANKVLG-LAMKSEWPIAEELKXL-EKVAVNVGB----- 111

Qy   225 ISNFLHADVNPNVKGAKNVMT-LMHLYAC-DVDPRIVAALGEVENDEGLGANAYNLV 282
Db   112 -----DGNHIPLAGVHDNMGTGPLMYATATKNKTAIMDRMIBLGADVAGARNNDNYNV- 163

Qy   283 DSEGNLPPLHAAKNCTGDKLKLCMEKTFTDITANFANOSPLHIITOKPDCSVLDIEE- 341
Db   164 -----LHTAAMYSRDVDVKLLLTTRGVDPFFSTGGRSQTAVHLVSRRQTGTATNLRA 216

Qy   342 -FTSRNIIDFGL-VDGDGNPLHAHEHLPPVILKGMVDHVKNSEFOQLVNDPDYFGNTI 399
Db   217 LLAAAGKDRLKADGRGIPLLAAVESGNQMCRELL-----AAQTAEQLKATTANGDTA 271

Qy   400 AHYAVKNNKADTLTFNMLKASGADLVNRVVVRAPIHVASNSKANAVSLVSCGIDVNS 459
Db   272 LHLAARR--DVHMVRLVDYGTVNDVTQNSEGOTPLHIAAABGEDALLKYFYGVRASASI 329

Qy   460 QDVNGDTPLHIAVEGGSMTV-----LAVLN-----Q 486
Db   330 ADNQRTPLHLAAENGHAHVIEILLADKFASIFERTKOGSTLMHIASLINGHAECATMLFK 389

Qy   487 RGADVSVONNDGVTPLMSAAKYDIGIKAL--GSAKPNTKGEDTV-----AKSL 535
Db   390 KGVYLHPNKDGAHSIHATAAYGHGTGIINTLLOKGEKVDVTINDNYTALHIAVESAKPAV 449

Qy   536 MEDYKGFPTPLHFVAGGSRDTFRVRKNYEKCHDLATI---RAALMODRSG----- 583
Db   450 VETLLGFGADVHRVGKLRTE-----PLHIAARVKDGRCALMLLSGASPNTLTD 500

Qy   584 -----GELVNLGPFESNILGSPNAKPLQHIOGANFPQSFPARRGIVSSHNHVM 631
Db   501 DCLTPVHVAARHGULATMLQLEDE-GDP-----LYKSNTGETPLHWACRACHPDIV 551

Qy   632 KDILNFYGDSDLHP-----SERGYNAM-----QYAALFGDKAEVOMKLAKSA 672
Db   552 RHLETYKEK-HGPDKAATTINSVNEEDGALTALHYTCOITKEEVKIPESDKOIVRMJLENG 610

Qy   673 -----KPSD-----LNFKTSATPTPLINACLAR 694
Db   611 ADVTLQTKTAETAIFYCAVAGNNDVLMEMI SHMNPTDIQAMNRQSSVGWTPLLIACHR 670

Qy   695 GDNEVREGLVGQG-IDINORMGSKNTVLHYAISKG-----DSFLVOKILAHTGVVDVNC 748
Db   671 GHMELVNLLIANHARDVV---FPTTEGR SALHAAERGTHVCVDALLTNKAF-----INS 721

Qy   749 ENNLGOPTPLHAVEGGDPKITVSSILK-AGAVAVNRLLDNGRSVLSSTATVPGRKEKGVLGIV 807
Db   722 KSRRVRTALHLAAMNGETHLVKVELIKDHNAVIDILTIRKQTPHLHAASAQME-----VC 776

Qy   808 NKLLDRGADINLQGD 822
Db   777 QLLELGCANIDATDD 791
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RESULT 8
US-10-108-260A-4122
; Sequence 4122, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:

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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560a1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4122
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4122

```

Query Match	8.5%	Score 364.5	DB 15	Length 919
Best Local Similarity	24.0%	Pred. No. 6.1e-27		
Matches 184	Conservative 95	Mismatches 283	Indels 205	Gaps 31
QY	170	AVLGKNEIKE-----EWLTSGPVRDIADRIIVASKGDLSEDQVEEILDIIF	215	
DB	24	AFLGDAEIELLILSGARVNAKNWLT-----PLH-----RAVASRS-----EEAVQVLI	69	
QY	216	MNESIEAEGISN-----PLHADVNNPVKGAKNVMTLMEHLVYACDVPRIIV-----KAL-GEVE	268	
DB	70	KHSADVNAKDKNQWTFPLHVAANAARCAEVIIPLLISSVNVSDRGKRTALHHAALNGHVE	129	
QY	269	-----NDEGDLGANAY-----NVLDEGNLPLHAA	294	
DB	130	MYNLLAKGANINAFDKDRRALHWAAYMGHLDVVALLINHGAEVTCDDKKGYTFLHAA	189	
QY	295	KNCTGDKLK-----LC-----MEKTKTFIDITANFANQ-----S	323	
DB	190	SNGQINVVKGHLNLGVFEIDENVYNTALHIAACYNGQDAVVNELIIDYGANVQPNNGFT	249	
QY	324	PLHIITQKPCSVLDIEFTSRNLDGVLVDGQKQPLHHAVEHLPPVILKGVMDH-----V	379	
DB	250	PLHFAAASHT-GALCELLVNGADVNIQSKDGKSPLLHMTAVH-----GRFTRSQTLI	301	
QY	380	KNSSBFQDLVNDPDYFGNTIIAHYAKVKNADLTLPMLKASGADLNVNVVGRAPIHVAS	439	
DB	302	QNGEIDCDVKD-----GNTPLHVAARTVGH-----LLINTLRTSGADTAKCGIHSMFPLHAA	355	
QY	440	SNGKANAVSGLVSCGIDVNSDVNGDTPHLHIAVEGGSGMETVLAVLNQRGADVSQVNDGV	499	
DB	356	LNAAHDCCKRLSSGFEIDTPKFGRTCLHAAAAGNVCEI-KLQSSGADPHKXDKGR	414	
QY	500	TPWLGAAYKGDIGVILKALGSAPKNIKEDTVAKSLLMEDYKGTPLHFVAG-----	550	
DB	415	TPHLYAANAACHFCHTETLVTTGANVNETD-----DW-GRTALHYAAASDMDRDKTI	464	
QY	551	-GSGRDTFRVVRKNYKCHDLATIRAAI-----MDRSGGELVN-----LGDF	592	
DB	465	LGNAHDN-----SEELERARELKEENTLCLEFLONDANPSIRDKGYNSIHYYAAAYGR	520	
QY	593	ESENILGSPNAKFLQHIQSANFGFSPARRGIVSSNNHNMKDIILNFVCGDSLHLPSERGYN	652	
DB	521	QCLELL-----LERTNSGFEESDGSATKS-----PLHL-----	548	
QY	653	MQVAALFGDKEAVKMLAKSPDSLINFKTSATPTPLMLACLRGDNEVRGLVQGHGIDIN	712	
DB	549	---AAYNGHQALEVLLQSL--VOLDIRDEKGRGTALDLAAFKRGHTCEVALLNP-GASIF	602	
QY	713	QWGSQKNTLVHLYASKDSFLVOKIL--AHTGVGVNCCNNLQOTPLHLHVRGGDPKIVS	770	
DB	603	VKDNVTKRTPHSAVINGHTLCRLLLLEIADNPENDVDKAKQOTPLMLAVAYGHIDAVS	662	
QY	771	SLLKAGAVNRLDDNRSVLSSAIVPGKEKGVILGINVKLLDRGADI	817	
DB	663	LLLEKEANVDTVDLGCTALHRTGIMTGH-----CYOMLLEOBVSI	704	

RESULT 9
US-10-369-978-6
; Sequence 6, Application US/10369978

```

; Publication No. US20030152991A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Walker, Richard G.
; APPLICANT: Willingham, Aaron
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A Eukaryotic Mechanosensory Transduction Channel
; FILE REFERENCE: 02307E-097600US
; CURRENT APPLICATION NUMBER: US/10/369,978
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US/09/392,812A
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: amino acid sequence derived from nompC genomic
; OTHER INFORMATION: sequence
US-10-369-978-6

```

Query Match	8.1%;	Score 351;	DB 14;	Length 1709;
Best Local Similarity	21.1%;	Pred. No. 1.4e-15;		
Matches	196;	Conservative 134;	Mismatches 326;	Indels 272; Gaps 38;
Qy	108	QPPIVODSNLYSISGG-----VPOBAQYDAAA---RAGGPKFLYGPYTFSGNGQIMDF	158	
Db	50	RPPL-RRSSTHLOIGKNSRIIFVQKPSRDSVTPDPRLGKPLFRESLTSHASHEEMSS	108	
Qy	159	EPDTPMPDVNRNAVILGNKEIKEEWLTTTSGPVVDI-----ADR-----IVASGDGL	202	
Db	109	E-DLAMADPQTILYPAK-RDEWANVSEIETIKRGSDFSMADNHGFTAFLLAVKAGKDOI	166	
Qy	203	SEDOVE-----ETLDIIFMNESEIAEGISNP-----LHAD	233	
Db	167	VDKMIKRGARVDYSTKQGRNATHIAAMYGSVETLEILIKRYSSELLKAGGPKQLAIHVA	226	
Qy	233	VDNNPVKAGKNVMTLMLHYVACDVPDRIKALGEVDEGDL-----GANAYNVL-	282	
Db	227	CERKSKKAPPIVKRILE-----DTDQRM-----AEDGGSPLFIHLAFKFGNVIVELL	275	
Qy	283	-----DSEGNLPLHAAKNCTGDKLKLCKMEKTKTDP---TDANFAN---QSPL	325	
Db	276	SGPSSDEQTRKADGNGDTLLHAAAR--SGN-----IEAVRTAIAAGCDNAKVQNRVGTPL	328	
Qy	326	HIITQPCDGSVLD-----IEEPTSRNL-----DFGLVDGDGKNPLHVAHEHLPPV	370	
Db	329	H-----ECLTVGTQKGYAEVGDQNMLIKMFKLADANIHKDEKTPVHVAERGDTS	382	
Qy	371	ILKGVMDHVKNSSFPQDLVNDPDYFGNTIAHYA-----VKNKNADL	411	
Db	383	MVESLID-----KFGGSIRARTRDGSTLLHIAACSGHTSTALAFKRVPLFPNPKKGAL	436	
Qy	412	TL-----FN-----MLKASGADLNVRNVGGRAPIHVASNGKANAVSLVSCGIDVN--	458	
Db	437	GLHSAAAAGFNDVVRKMLIARGTIVDVRTRDNYTALHVAVQSGKASVVETLLGSGADIHVK	496	
Qy	459	-SDVNGDTPHLIAVEGGSMETVLAVLNQRGADVSVQNNDGVPMLSAAYKGDIGVIKAL	517	
Db	497	GGEHMDETCLHIAARSGNKDIML--LLDENADSKISSEKIGETPLQVAASKCNFEAASMI	554	
Qy	518	GSAPNIKGBDYTVAKSLLMEDYKGTPLPHFVAGGGR-----DTRFVRVK--NYEKCHD	569	
Db	555	LKHLSEVLITQELKEHVNHRTNDGFTALHYAAIEQORQLHPFGGEDAKLNLLLIDYGGMVE	614	
Qy	570	LATIR-----AALMODRSGGELVNLGDPESENILGSPNAKFLQHSANFGFSPARRGIVS	625	
Db	615	MPSLNANETAMHWAARSGNQAVLLA---MVNKKIAGAVQIVQNKQKN--GWSPLLEACAR	670	
Qy	626	SNNFNVKMDIL-----	635	

Db 671 GHSGVANILLKVLVLCVGPFGPRLQGRGYWTRTRARVTVFWLQYQGYWARTRTRTRA 730
QY 636 -----NFVGD---SLHLPSEBGRYNAMOVAALFGDKKAVKM 667
Db 731 RATCPGLQDQGYWARTRTRKVTVPRLGLDHHARIDVDEMGRTALHLAAPNGHLSVLHL 790
QY 668 LAKSAKPSDLNFKTSATPTPLNLACLRGDNVVRGLVQGHGIDINQRMGSDKNTVLHYAI 727
Db 791 LLQ--HKAFFNSKSKTGEAPLHLAAQHGHVKNVNLVQDGHGAAL-EAITLNDQTALHFAA 847
QY 728 SKGDSFLVKILAHGTVDVNCENNLGOTPLHLHVEGGDPKIVSLLKA-----GAVNRLD 783
Db 848 KFGQLAVSQTLA--LGANPNARDKQGTPLHLAENDFPDVVKLFLKORNNRSVLTAID 906
QY 784 DNGRSVLSSAIVPGRKEKGLVGNKLL 811
Db 907 HNGFTCAHIAAM-----KGLAVVRELM 929

RESULT 10

US-10-479-764-23
; Sequence 22, Application US/10479764
; Publication No. US20050027103A1
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. Tom; WARREN, Bridget A.;
; APPLICANT: HONCHELL, Cynthia D.; RICHARDSON, Thomas W.;
; APPLICANT: ELLIOTT, Vicki S.; CHAWLA, Narinder K.;
; APPLICANT: YUE, Henry; BAFTA, Sajeev;
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.;
; APPLICANT: FORSYTHE, Ian J.; BURFORD, Neil;
; APPLICANT: EMBELING, Brooke M.; SANJANWALA, Madhusudan M.;
; APPLICANT: KHAN, Farah A.; LU, Dzung Aina M.;
; APPLICANT: HAFALIA, April J.A.; NGUYEN, Damiel B.;
; APPLICANT: YANG, Junming; LI, Joana X.;
; APPLICANT: BECHA, Shanya D.; YAO, Monique G.;
; APPLICANT: GIETZEN, Kimberly J.; LUO, Wen;
; APPLICANT: UBE, Ernestine A.; ISON, Craig H.;
; APPLICANT: LASEK, Amy W.

; TITLE OF INVENTION: STRUCTURAL AND CYTOSKELETON-ASSOCIATED PROTEINS

; FILE REFERENCE: PP-1007 USN
; CURRENT APPLICATION NUMBER: US/10/479,764
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/US02/17956
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/296,865
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/296,878
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/298,664
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/300,149
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/302,340
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/303,481
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/305,059
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/343,557
; PRIOR FILING DATE: 2001-12-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 1094
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 8013295CD1

US-10-479-764-22

Query Match 8.1%; Score 350; DB 17; Length 1094;
Best Local Similarity 25.7%; Pred. No. 8.5e-16;

Matches 127; Conservative 75; Mismatches 206; Indels 86; Gaps 17;
QY 323 SPLHIITQKPCDSCVLDIEBFTSRNLDGVLVDGKGNPLHHAHVEHLPEVLKGVMDHVKN 382
Db 23 TPLHIACKNRKIKMEL--LLKHGASIQAVTESGLTPIHVA-----AFMGHVNIV 70
QY 383 SEFQD---LVNDPDYFGNTIAHYAVRNKNADLTLFNMLKASGADLNVNVRVGRAPIHVAS 439
Db 71 SOLMHGASPTNTNVRGETALHMAARSQGAEEVRY--LVQDGAQVEAKAKDDQDTPLHISA 128
QY 440 SNGKANAVSGLVSCGIDVNSQVNGDTPLHIAVEGGSMETVLAIVLQRGADVSQVNDGV 499
Db 129 RLGKADIVQOLLQOQGASPNAAATTSYTPLHLSAREGH-EDVAAFLDLHGASLSTITTKKGF 187
QY 500 TPLMSAAKYGDIGIKAL--GSAKPNIKGEDTVAKSLLMEDYKGFTHFVAGGSRDTF 557
Db 188 TPLHVAAYKYLEVANLLLOKSASPDAAK-----SGLTPLHVA--HYDNQ 232
QY 558 RVVRKNYKCHDIATIRAAALMQDRSGGELVNLGDFESENILGSPNAKFLQHIQSANFGFS 617
Db 233 KV-----ALLLLDQG-----ASPHA-----AAKNGYT 254
QY 618 PARRGIVSSNNHNMKDIINPVGDSLHLPSERGNAMQVAALFGDKKAVKMLAKSPSOL 677
Db 255 PLHIAAKNQMDIATTLLEYGADA-NAVTRQGTASVHLAAQEGHVDVMSLLL--GRNANV 311
QY 678 NFKTSATPTPLNLACLRGDNVVRGLVGOHG-IDINQRMGSDKNTVLHYAISKDSFLVQ 736
Db 312 NLSNKSGLTPLHLAAQEDRVNVAEVLVNOGAHVDAQTRMG---YTPLHVGCHYGNIKIVN 368
QY 737 KILAHTGVDVNCENNLGOTPLHLAVRGDPKIVSSLLKAGAVNRLDDNGRSVLSAIVP 796
Db 369 FLQLHS-AKVNAKTKNGYTPLHQAQQGHTHIINVLQNNASPNELTVNGNTALGIA--- 424
QY 797 GRKEKGLVGNKLL 810
Db 425 --RRLGYISVVDTL 436

RESULT 11

US-10-205-194-117
; Sequence 117, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 117
; LENGTH: 1762
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Ankyrin isoform
US-10-205-194-117

Query Match 8.0%; Score 345.5; DB 14; Length 1762;
Best Local Similarity 24.8%; Pred. No. 3.6e-15;
Matches 169; Conservative 95; Mismatches 284; Indels 133; Gaps 26;
QY 184 TSGPVRDIADRVASKGDLSEDOVEEILDIIFWNES-----ETAEGLSNPLH----- 230
Db 191 TKGKVLPAHIAARKDD-----TKAAALLQNDTNADIESKSGFT-PLHTAAHYGNIN 243

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 18:45:13 ; Search time 50 Seconds
(without alignments)

1599.123 Million cell updates/sec

Title: US-10-701-038-2

Perfect score: 4310

Sequence: 1 PGSDIQDSQDQEQDQDQ.....DRGADINLGDHNLFDQCL 831

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	391.5	9.1	1856	B35049	ankyrin 1, erythro
2	391.5	9.1	1880	A35049	ankyrin 1, erythro
3	390.5	9.1	1881	SJHUK	ankyrin 1, erythro
4	382.5	8.9	1848	S37771	ankyrin, erythrocy
5	381.5	8.9	1862	I49502	ankyrin - mouse
6	378.5	8.8	1765	T42714	ankyrin 3, splice
7	378.5	8.8	1940	T42715	ankyrin 3, splice
8	378.5	8.8	1943	T42713	ankyrin 3, splice
9	378.5	8.8	1961	T42716	ankyrin 3, splice
10	377.5	8.8	4377	A55575	ankyrin 3, long sp
11	368.5	8.5	3924	S37431	ankyrin 2, neurona
12	345	8.0	791	T42691	hypothetical prote
13	344	8.0	1401	S11527	alpha-latrotoxin p
14	342	7.9	934	H71274	probable ankyrin -
15	339.5	7.9	1549	T13940	ankyrin - fruit fl
16	334.5	7.8	2039	T15347	ankyrin-related un
17	321	7.4	1411	S30355	alpha-latroinsecto
18	313.5	7.3	1062	T14151	inv protein - mous
19	313.5	7.3	1062	T30255	inversin - mouse
20	269.5	6.3	1184	T00253	gene Ankhzn protei
21	269	6.2	337	T46445	hypothetical prote
22	263	6.1	1188	T19552	hypothetical prote
23	255	5.9	426	AE2149	hypothetical prote
24	254	5.9	633	T27499	hypothetical prote
25	250	5.8	907	I50404	p50B/p97 (lyt-10)
26	249	5.8	1031	T43458	hypothetical prote
27	227	5.3	1423	I37275	death-associated p
28	225.5	5.2	643	D86167	protein F21B7.27 [
29	225	5.2	557	T46507	hypothetical prote

hypothetical prote
hypothetical prote
ankyrin-like prote
hypothetical prote
hypothetical prote
NF-kappa-B p50 sub
hypothetical prote
hypothetical prote
ankyrin-like prote
transcription fact
ankyrin-like prote
hypothetical prote
hypothetical prote
hypothetical prote
notch protein - fr
notch protein homo

ALIGNMENTS

RESULT 1

B35049

ankyrin 1, erythrocyte splice form 3 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2, erythrocyte

C;Species: Homo sapiens (man)

C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998

C;Accession: B35049

R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A;Title: cDNA sequence for human erythrocyte ankyrin.

A;Reference number: A35049; UID:90175370; PMID:1689849

A;Accession: B35049

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1856 <LAM>

C;Genetics:

A;Gene: GDB:ANK1; ANK

A;Cross-references: GDB:118737; OMIM:182900

A;Map position: 8p11.2-8p11.2

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing

F;2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
F;2-1513.1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F;44-76/Domain: ankyrin repeat homology <AN01>
F;77-109/Domain: ankyrin repeat homology <AN02>
F;110-142/Domain: ankyrin repeat homology <AN03>
F;143-171/Domain: ankyrin repeat homology <AN04>
F;172-204/Domain: ankyrin repeat homology <AN05>
F;205-237/Domain: ankyrin repeat homology <AN06>
F;238-270/Domain: ankyrin repeat homology <AN07>
F;271-303/Domain: ankyrin repeat homology <AN08>
F;304-336/Domain: ankyrin repeat homology <AN09>
F;337-369/Domain: ankyrin repeat homology <AN10>
F;370-402/Domain: ankyrin repeat homology <AN11>
F;403-435/Domain: ankyrin repeat homology <AN12>
F;436-468/Domain: ankyrin repeat homology <AN13>
F;469-501/Domain: ankyrin repeat homology <AN14>
F;502-534/Domain: ankyrin repeat homology <AN15>
F;535-567/Domain: ankyrin repeat homology <AN16>
F;568-600/Domain: ankyrin repeat homology <AN17>
F;601-633/Domain: ankyrin repeat homology <AN18>
F;634-666/Domain: ankyrin repeat homology <AN19>
F;667-699/Domain: ankyrin repeat homology <AN20>
F;700-732/Domain: ankyrin repeat homology <AN21>
F;733-765/Domain: ankyrin repeat homology <AN22>
F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 9.1%; Score 391.5; DB 2; Length 1856;
Best Local Similarity 26.0%; Pred. No. 1.2e-14;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

Qy 821 GDNILFDQ 829
Db 800 DKHRMSFPE 808

RESULT 3

SUHUK

N;Ankyrin 1, erythrocyte splice form 1 - human
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
C;Contains: ankyrin 2.2
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S08275; A33219; PC2220; A35443
R;Lux, S.E.; John, K.M.; Bennett, V.
Nature 344, 36-42, 1990
A;Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure
A;Reference number: S08275; MUID:90158830; PMID:2137557
A;Accession: S08275
A;Molecule type: mRNA
A;Residues: 1-1881 <LJ1>
A;Cross-references: UNIPROT:P16157; EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702
A;Accession: A33219
A;Molecule type: protein
A;Residues: 2-7; 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753, 828-833, 'X', 835-855, 'X',
X', 1367; 1383-1427; 1601-1630; 1686-1698, 'D', 1700; 1763-1772 <LUX>
A;Note: 845-Arg and 1392-Thr were also found
R;Hermann, J.; Barel, M.; Frade, R.
Biochem. Biophys. Res. Commun. 204, 453-460, 1994
A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A;Reference number: PC2220; MUID:95071348; PMID:7526850
A;Accession: PC2220
A;Molecule type: protein
A;Residues: 910-929 <HER>
R;Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A;Reference number: A35443; MUID:90285190; PMID:2141335
A;Accession: A35443
A;Molecule type: protein
A;Residues: 'X', 5, 'X', 7-12, 403-417, 'X', 419-422, 'H', 424, 'LQ', 797-800, 'L', 802-814, 862-863,
C;Genetics:
A;Gene: GDB:ANK1; ANK
A;Cross-references: GDB:118737; OMIM:182900
A;Map position: 8p11.2-8p11.2
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing; phosphoprotein
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
F;2-827/Region: anion exchange protein binding
F;44-76/Domain: ankyrin repeat homology <AN01>
F;77-109/Domain: ankyrin repeat homology <AN02>
F;110-142/Domain: ankyrin repeat homology <AN03>
F;143-171/Domain: ankyrin repeat homology <AN04>
F;172-204/Domain: ankyrin repeat homology <AN05>
F;205-237/Domain: ankyrin repeat homology <AN06>
F;238-270/Domain: ankyrin repeat homology <AN07>
F;271-303/Domain: ankyrin repeat homology <AN08>
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F;370-402/Domain: ankyrin repeat homology <AN11>
F;403-435/Domain: ankyrin repeat homology <AN12>
F;436-468/Domain: ankyrin repeat homology <AN13>
F;469-501/Domain: ankyrin repeat homology <AN14>
F;502-534/Domain: ankyrin repeat homology <AN15>
F;535-567/Domain: ankyrin repeat homology <AN16>
F;568-600/Domain: ankyrin repeat homology <AN17>
F;601-633/Domain: ankyrin repeat homology <AN18>
F;634-666/Domain: ankyrin repeat homology <AN19>
F;667-699/Domain: ankyrin repeat homology <AN20>
F;700-732/Domain: ankyrin repeat homology <AN21>
F;733-765/Domain: ankyrin repeat homology <AN22>
F;766-798/Domain: ankyrin repeat homology <AN23>

F;828-1382/Domain: 62K #status predicted <DOM2>
F;828-1382/Region: spectrin binding
F;1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 9.1%; Score 390.5; DB 1; Length 1881;
Best Local Similarity 26.0%; Pred. No. 1.4e-14;
Matches 174; Conservative 100; Mismatches 246; Indels 149; Gaps 31;

Qy 194 RIVASKGLDSEDQVERILDIFMNESEIEAGISNPLHADVDNNPVK-----GA----- 241
Db RLLDRGAQIETTKDEL-----TPLHCAARNGHVRISEILLDHGAPIQA 300
Qy 242 --KNVMTLMLHYVACD-VDPRIKALGEVNDGDLGANAYNVLDSGNLPLHAAKNCT 298
Db KTKNGLSPITHMAAQGDHLD--CVRLLLQYDAEIDDI-----TLD---HLTPLHVAHCG 349
Qy 299 GDKL-KLCMEKYTKYDFIDTANFANQSPHIIITQKPCSVLIDIEFTSRNLDLFGVDDGK 357
Db HHRVAKVLLDKGAKPNRSRLN--GFTPLHACKNHVRVMEILLKTKGASID--AVTESGL 405
Qy 358 NPLHHA--VEHLPPV--ILKGVMDHVKNSSSEFQDLVNDPDYE-----GNT-IAHYAVKN 407
Db TPLHVASFMGHLPIVKNLQORGASPNVNVK-----VETPLHMAARAGHTEVAKYLQNK 460
Qy 408 NADLTLENMLKASGADLNVNVVGRAPIHVASSNGKANAVSGILVSCGIDVNSQDVNGDTP 467
Db -----AKVNAKAKDDQTPHCAARIGHTNMVKKLENNANPNLATTAGHTP 506
Qy 468 LHIAVEGGSMETVLAVLNORGADVSNQNDGVTTPMLSAKYDIGIVKAL--GSAKPNIK 525
Db LHIAAREGHVETVLALL--EKEASQACMTKGGFTPLHVAAYKGVKRVVAELLERDAHPNA 565
Qy 526 GEDTVAKSLLMEDYKGTPLHVFVAGGSDRTPRVVRKNVEKCHDLATIRAALMQDRSGGE 585
Db GKN-----GLTPLHVAHNNLDIVKL----- 587
Qy 586 LVNLGDFESENTLGSPNAKFLQIQAANFGSPARRGIVSSNNHNMKDLINLVGDSILHLP 645
Db LPRG-----GSP-----HSPAWN-GYTPHLHAAKQNOVEVARSLLQY-GGSANAE 631
Qy 646 SERGYNAQVAALFGDKEAVKMLAKSPKSDLNFKTSATPTPLNLAACLDGNEVVRGLVG 705
Db SVQGVTPPLHAAQEGHAENVALL--SKOANGNLGNKSGLTPLHVAQEGHVPVADVLI- 688
Qy 706 QHG--IDINQRMGSKNTVLHVAISKGDSFLVKILAHGTGVNVCNNIGOTPLHLAVEG 763
Db KGVWVDATTRMG--YTPHVAHYGNLKLKFLQHQ-ADVNAKTLGYSFHLQAQQ 744
Qy 764 GDPKIVSYSLKAGAVNRLDNGRSVLSSAIVPGRKEKGLGIVNKL---LDRGADINLD 820
Db GHTDITVTLKNGASPNVSSDGTTELAIA-----KRLGVISVTDVLKVVTDTSFVLVS 799
Qy 821 GDNILFDQ 829
Db DKHRMSFPE 808

RESULT 4

S37771

ankyrin, erythrocyte - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: S37771

R;Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.

J. Biol. Chem. 268, 9533-9540, 1993

A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found

A;Reference number: S37771; MUID:93252825; PMID:8486643

A;Accession: S37771

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1848 <BIR>

A;Cross-references: UNIPROT:Q61302; EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311

C;Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing
F:48-80/Domain: ankyrin repeat homology <AN01>
F:81-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN06>
F:242-274/Domain: ankyrin repeat homology <AN07>
F:275-307/Domain: ankyrin repeat homology <AN08>
F:308-340/Domain: ankyrin repeat homology <AN09>
F:341-373/Domain: ankyrin repeat homology <AN10>
F:374-406/Domain: ankyrin repeat homology <AN11>
F:407-439/Domain: ankyrin repeat homology <AN12>
F:440-472/Domain: ankyrin repeat homology <AN13>
F:473-505/Domain: ankyrin repeat homology <AN14>
F:506-538/Domain: ankyrin repeat homology <AN15>
F:539-571/Domain: ankyrin repeat homology <AN16>
F:572-604/Domain: ankyrin repeat homology <AN17>
F:605-637/Domain: ankyrin repeat homology <AN18>
F:638-670/Domain: ankyrin repeat homology <AN19>
F:671-703/Domain: ankyrin repeat homology <AN20>
F:704-736/Domain: ankyrin repeat homology <AN21>
F:737-769/Domain: ankyrin repeat homology <AN22>
F:770-802/Domain: ankyrin repeat homology <AN23>

Query Match 8.9%; Score 382.5; DB 2; Length 1848;
Best Local Similarity 26.2%; Pred. No. 4e-14;
Matches 180; Conservative 98; Mismatches 259; Indels 151; Gaps 33;

QY 221 IAGISNPLHADVNNPVKAKNVTLMHLVYACDVDPRIKALGEVENDEGLGANAYN 280
DB 156 LQGHENVV-AHLINVTGK-KVRLPALHIAARN-DTRTAAVL--LQNDPNP-----D 204

QY 281 VLDSEGNPLHHAANKCTGDKLCKMEKTKTDFIDTANFANQ---SPLHIITQKDCSVL 337
DB 205 VLSKTGFTPLHAAHYENLVAQLLNKRG-----SVNFTPQNGITPLHIAARRGNVIMV 259

QY 338 DI-----EEFT-----SRN-----LDFG-----LVDGDKNPLHHA--- 363
DB 260 RLLDRGAQIETRTKDELTPHCAARNGHVRISSEILLDHGAPIQAKTKNGLSPIHWAQ 319

QY 364 -----VEHLPVILKGMVMDHVKNSSEFQDLVNDPD---YFNTIA 400
DB 320 DHLDCVRLLLQVNAEIDITLDHLTPHVAACHGHRHVAKVLLDKGAKPNSALNGFTPL 379

QY 401 HYAVKKNADLTFLFMKASGADLNVNVRGAPIHVASSNGKANAVSGLVSCGIDVNSQ 460
DB 380 HTACKKNH--IRVMELLKTKGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVS 437

QY 461 DVNGDTPHIAVEGGSMETVLAVLNQRGADVSQNNNDGVTTPMLSAKYGDIGVICAL--G 518
DB 438 NVKVTETPLHMAARAGHTE-VAKYLLQNKAKAKAKDDQTPPLHCAARIGHTGMVLLLEN 496

QY 519 SAKPNT-----KGEDTVAKSLLMED-----YKGFPTPLHFVAGGSGSRDTF 557
DB 497 GASPNLATTAGTTPHIAAREGHVDTLALLEKEASQACWTKKGFTPLHVAKYGK--V 553

QY 558 RVVRKNYKCHD-----LATIRAAIMODRSGGELVNLGDFESENIL---GSPNAK 604
DB 554 RLAEALLLE--HDAHPNAAGKNGLTPLHVAVHNHL--DIVKL-----LLPRGGSP--- 599

QY 605 FLOHIOANEGFSPARRGIVSSNHNVMKDILANFVGDLSLHLPSERGYNAMQVAALEGKEA 664
DB 600 ---HSPAWN-GYTPHIAAKQNOIEVARSLQF--GGSANAEVSQGVTPPLHIAAQEGHTEM 654

QY 665 VKMLAKSAKPSDLNFKTSATPTPLNLACLRGDNEVVRGLVGQHG--IDINQRMGSDKNVT 722
DB 655 VALLLL--SKQANGNLGNKSLTEPLHLVSOBHGHPVADVLI-KHGVTVDATTRMG---YTP 708

QY 723 LHYAISKGSFSLVQKILAHGTGVVNCENNLGQTPHLAVEGGDPKIVSSILLKAGAVVRL 782
DB 709 LHVASHYGNIKLVKFLLOHQ-ADVNNAKTGLVSPHQAQOQGHDTIVTLLKNGASPNEV 767

783 DDNGRSVLSAIVPGRKEKGVLGIVNKL 810
DB 768 SSGTTPATA-----KRLGVIISTDVL 790

RESULT 5
149502
ankyrin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49502
R:White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory domain
A:Reference number: I49502; MUID:92345717; PMID:1386265
A:Accession: I49502
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1862 <RES>
A:Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:cl91940
C:Genetics:
C:Gene: Ank-1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:40-72/Domain: ankyrin repeat homology <AN01>
F:73-105/Domain: ankyrin repeat homology <AN02>
F:106-138/Domain: ankyrin repeat homology <AN03>
F:139-167/Domain: ankyrin repeat homology <AN04>
F:168-200/Domain: ankyrin repeat homology <AN05>
F:201-233/Domain: ankyrin repeat homology <AN06>
F:234-266/Domain: ankyrin repeat homology <AN07>
F:267-299/Domain: ankyrin repeat homology <AN08>
F:300-332/Domain: ankyrin repeat homology <AN09>
F:333-365/Domain: ankyrin repeat homology <AN10>
F:366-398/Domain: ankyrin repeat homology <AN11>
F:399-431/Domain: ankyrin repeat homology <AN12>
F:432-464/Domain: ankyrin repeat homology <AN13>
F:465-497/Domain: ankyrin repeat homology <AN14>
F:498-530/Domain: ankyrin repeat homology <AN15>
F:531-563/Domain: ankyrin repeat homology <AN16>
F:564-596/Domain: ankyrin repeat homology <AN17>
F:597-629/Domain: ankyrin repeat homology <AN18>
F:630-662/Domain: ankyrin repeat homology <AN19>
F:663-695/Domain: ankyrin repeat homology <AN20>
F:696-728/Domain: ankyrin repeat homology <AN21>
F:729-761/Domain: ankyrin repeat homology <AN22>
F:762-794/Domain: ankyrin repeat homology <AN23>

Query Match 8.9%; Score 381.5; DB 2; Length 1862;
Best Local Similarity 26.0%; Pred. No. 4.6e-14;
Matches 179; Conservative 101; Mismatches 257; Indels 151; Gaps 33;

QY 221 IAGISNPLHADVNNPVKAKNVTLMHLVYACDVDPRIKALGEVENDEGLGANAYN 280
DB 148 LQGHENVV-AHLINVTGK-KVRLPALHIAARN-DTRTAAVL--LQNDPNP-----D 196

QY 281 VLDSEGNPLHHAANKCTGDKLCKMEKTKTDFIDTANFANQ---SPLHIITQKDCSVL 337
DB 197 VLSKTGFTPLHAAHYENLVAQLLNKRG-----SVNFTPQNGITPLHIAARRGNVIMV 251

QY 338 DI-----EEFT-----SRN-----LDFG-----LVDGDKNPLHHA--- 363
DB 252 RLLDRGAQIETRTKDELTPHCAARNGHVRISSEILLDHGAPIQAKTKNGLSPIHWAQ 311

QY 364 -----VEHLPVILKGMVMDHVKNSSEFQDLVNDPD---YFNTIA 400
DB 312 DHLDCVRLLLQVNAEIDITLDHLTPHVAACHGHRHVAKVLLDKGAKPNSALNGFTPL 371

QY 401 HYAVKKNADLTFLFMKASGADLNVNVRGAPIHVASSNGKANAVSGLVSCGIDVNSQ 460
DB 372 HTACKKNH--IRVMELLKTKGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVS 429

QY 461 DVNGDTPHIAVEGGSMETVLAVLNQRGADVSQNNNDGVTTPMLSAKYGDIGVICAL--G 518

Db 430 NVKVTETPLHMAARAGHTE--VAKYLLQNKAKANAKAKDDQTPHLHCAARIGHTGMVKLLLEN 488
QY 519 SAKPNI-----KGEDTVAKSLMED-----YKGFTHLFFVAGGSRDTP 557
Db 489 GASPNTATTAGHTPLHTAAREGHVDVTALALLEKEASQACMTKGTPLHVAAYKYGK--V 545
QY 558 RVVRKNYEKCHD-----LATIRAALMQDRSGGELVNLGDFESENIL--GSPNAK 604
Db 546 RLAEELLE--HDAHNPNAAGKNGLTPLHVAVHNNL--DIVKL-----LLPRGSP-- 591
QY 605 FLOHIQSANFGSPARRGIIVSSNNVNMKDILNFVGDLSHLPSERGNAMQVAALFGDKEA 664
Db 592 ---HSPAWN--GYTPLHTAARQONQTEVARSLQY--GGSANAESVQGVTPHLAAQEGHTEM 646
QY 665 VKMLAKSAKPSDLNFKTSATPTPLNLAACLRGDNVVRGLVQGH--IDINORMGSDKNTV 722
Db 647 VALLE--SKQANGMLGNKSLGTPHLVVSQEG--HVLVADVLKHGVTVDATTRMG---YTP 700
QY 723 LHYAISKGDSPFLVOKILAHGTGVNVCENNIGQTPHLHVAEGGDPKIVSSLLKAGAVVNR 782
Db 701 LHVASHYGNIKLVKFLQHQ--ADVNAKTKLGYSPLHQAQCGHTDIIVTLLKNGASPNV 759
QY 783 DNGRSVLSAIVPGRKEKGVIGVKNL 810
Db 760 SSNGTTPLAIA-----KRLGVISVTDVL 782

RESULT 6
T42714
ankyrin 3, splice form 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42714
R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I
J. Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A;Reference number: 222237; MUID:95340633; PMID:7615634
A;Accession: T42714
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1765 <PET>
A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710551; PIDN:AAB01605
A;Experimental source: strain C57BL/6J; kidney
C;Genetics:
A;Gene: Ank3
A;Map position: 10
A;Introns: 1587/1
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing

Query Match 8.8%; Score 378.5; DB 2; Length 1765;
Best Local Similarity 25.7%; Pred. No. 6.4e-14;
Matches 175; Conservative 98; Mismatches 275; Indels 133; Gaps 27;

QY 184 TSGPVRDIADRIIVASKGDLSEDQVEILDIIFNNE-----EIAEGISNPLH----- 230
Db 180 TKGKVRPLPALHIAARKDD-----TKAALLQNDTNADVSKSGFT-PLHIAHYGNIN 232
QY 231 -----ADVNNPVKAGNVMTLMHLVYACDVPRIYKALGEVNDGDLGANAIV 281
Db 233 VATLLNRAAAVDFT-----ARNDITPLH-VASKEGNANVMVKLL-----LDRGAK-IDA 279
QY 282 LDSEGNLPLHAAKNCTGDKLCKMEKTKTDFDTANFANQSPHLHIITQKPCDCLDIEE 341
Db 280 KTRDGLTPLHCGARSQHEQVVEMLDRSAPILSKTKN--GLSPLHMAQGDHLCVQL-- 335
QY 342 FTSRNLDFGLVDGDKGNPLHHAHEPLPPVILKGMVMDHKVNSSEFQDLVNDPDPFGNTIAH 401
Db 336 LLOHNVDPDVTNDYLTALHVAACHGHYKVAKVLLD--KKASPNAKALN-----GFTPLH 388
QY 402 YAVKNKNADLTFLNMLKASGADLNVRNVGRAPLHVASSNGKANAVSGLVSCGIDVNSQD 461

Db 389 IACK-KNR-IRVMELLKKGASIQAVTESGLTPIHVAAFMGHVNIVSQLMHGASPNVTN 446
QY 462 VNGDTPHLHVAEGSMETVLAVLNQBGADVSVQNNQDGTPLMLSAAKYGDIGVICAL--GS 519
Db 447 VRGETALHMAARSGQAE--VVRYLVQDGAQVEAKAKDDQTPHLHSARLGKADIIVQQLLQOG 505
QY 520 AKENI-----KGEDTVA-----KSLLMEDYKGTPLPLHFVAGGSRDTPR 558
Db 506 ASPNAATTSGYTPHLHAAAREGHEDVAAPLLDHGASLSITTTKGTPLPLHVAAYKYGKLEV-- 563
QY 559 VRKNYEKCHDLATIRAALMQDRSGGELVNLGDFESENILGSPNAKFLQHIQSANFGSP 618
Db 564 -----ASLLLOKS-----ASPD-----AGKSLGTP 584
QY 619 ARRGIVSSNNVNMKDILNFVGDLSHLPSERGNAMQVAALFGDKEAVKMLAKSAKPSDLN 678
Db 585 LHVAAHYDNQKVALLLD--QGASPHAAAKNGYTPHLHIAAKKNQNDIATSLLEYG--ADAN 641
QY 679 FKTSATPTPLNLAACLRGDNVVRGLVQGH--GIDINORMGSDKNTVHLHYAISKGDSPFLVOK 737
Db 642 AVTROGIAVSHLAAQEGHVDVMSLLSRNANVNLNKSGL--TPLHLA-AQEDRVNVAE 697
QY 738 ILAHTGVNVCENNIGQTPHLHVAEGGDPKIVSSLLKAGAVVNRLLDNGRSVLSAIVPG 797
Db 698 VLVNQGAVDAQTKMGYTPHLVGHYGNIKIVNFFLQHSKAVNAKTKNGYTLHQA----- 753
QY 798 RKEKGVIGVKNLDRGADIN 818
Db 754 -AQOQHTHIINVLQNNASPN 773

RESULT 7
T42715
ankyrin 3, splice form 3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42715
R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I
J. Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A;Reference number: 222237; MUID:95340633; PMID:7615634
A;Accession: T42715
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1940 <PET>
A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01605
A;Experimental source: strain C57BL/6J; kidney
C;Genetics:
A;Gene: Ank3
A;Map position: 10
A;Introns: 834/1
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing

Query Match 8.8%; Score 378.5; DB 2; Length 1940;
Best Local Similarity 25.7%; Pred. No. 7.5e-14;
Matches 175; Conservative 98; Mismatches 275; Indels 133; Gaps 27;

QY 184 TSGPVRDIADRIIVASKGDLSEDQVEILDIIFNNE-----EIAEGISNPLH----- 230
Db 180 TKGKVRPLPALHIAARKDD-----TKAALLQNDTNADVSKSGFT-PLHIAHYGNIN 232
QY 231 -----ADVNNPVKAGNVMTLMHLVYACDVPRIYKALGEVNDGDLGANAIV 281
Db 233 VATLLNRAAAVDFT-----ARNDITPLH-VASKEGNANVMVKLL-----LDRGAK-IDA 279
QY 282 LDSEGNLPLHAAKNCTGDKLCKMEKTKTDFDTANFANQSPHLHIITQKPCDCLDIEE 341
Db 280 KTRDGLTPLHCGARSQHEQVVEMLDRSAPILSKTKN--GLSPLHMAQGDHLCVQL-- 335
QY 342 FTSRNLDFGLVDGDKGNPLHHAHEPLPPVILKGMVMDHKVNSSEFQDLVNDPDPFGNTIAH 401


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Qy 231 -----ADVDNPNVKGAKNVMTLMHLVYACDVPRIVKALGEVNDGDLGANAYNV 281
Db 233 VATLLNRAAAVDFT---AENDITPLH-VASKEGNANVVKLL-----LDRGAK-IDA 279
Qy 282 LDSSEGNPLHHAANKCTGDKLCKMEKTKTDFIDTANFANOSPLHIITQKPCDSCVLIDEE 341
Db 280 KTRDGLTPLHCGARSQHEQVEMLLDRSAPILSKTKN--GLSPLHMAATQGDHLNVCVQL-- 335
Qy 342 FTSNLDPLGLVDGQKGNPLHHAHEHLPPVILKGMVDHVKNSSSEFQDLVNDPDYFGNTIAH 401
Db 336 LLQHNVPDVTNDYLTALHVAACHGHYKVAKVLLD--KASPNNAKALN-----GFTPLH 389
Qy 402 YAVKKNADLTFLFNLKASGADLVNVRNVGSRPHVASNGKANANASGLVSCGIDVNSQD 461
Db 389 IACK-KNR-IRVMELLLKHGASIQAVTESGLTPIHVAAFMGHVNIIVSOLMHHGASPNVTN 446
Qy 462 VNGDTPPLHIAVEGSGMETVLAVLNQRGADVSQVNDGVTPLMSAAKYDIDIGVIAL--GS 519
Db 447 VRGETALHMAARSQAE-VVRYLVQDGAQVEAKAKDDQTPPLHISARLGKADIVQQLLQOG 505
Qy 520 AKPNI-----KGEDTVA-----KSLMEDYKGTPLHFAVAGGSRDTPR 558
Db 506 ASPNAATTSYTPPLHIAAREGHEDVAAFLDGHGASLSITTKGFTPLHVAAYKGLV-- 563
Qy 559 VVRKNYEKCHDLATIRAAALMDRSRGGELVNLGDPSESNILGSPNAKFLQHIQSANFGFSP 618
Db 564 -----ASLLLOKS-----ASPD-----AGKSLTP 584
Qy 619 ARRGIVSSNNHVMKDILNFVGDLSLHLPSPERGYNAMQVAALFGDKEAVKMLAKSPDLN 678
Db 585 LHVAHYDQKVALLLLD-QGASPHAAAKNGYTPPLHIAAKKNQMDIATSLLEYG--ADAN 641
Qy 679 PKTSATPTPLNLAACLRGNEVVRGLVGQH-GIDINQRMGSDKNTVLHYVSKGDSFLVQK 737
Db 642 AVTRQGIASVHLAAQEGHVDVMSVLLSRNANVNLNKSGL---TPLHLA-AQEDRVNVAE 697
Qy 738 ILAHTGVVNCENNIGTPTPLHIAVEGGDPKIVSSLLKAGAVNRLDNGRSVLSSAIVPG 797
Db 698 VLNVQGAHVDAQTQMGYTPPLHVGHYGNIKIVNFIQLHSAKVNAKTKNGYTPALHQA----- 753
Qy 798 RKEKGVILGVNKLDRGADIN 818
Db 754 -AQQGTHIINVLQNNASPN 773

RESULT 10
A55575
N;Ankyrin 3, long 'splice form - human
N;Alternate names: ankyrin G
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55575
R;Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A;Title: Ankyrin-G. A new ankyrin gene with neutral-specific isoforms localized at the ax
A;Reference number: A55575; MUID:95138209; PMID:7836469
A;Accession: A55575
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4377 <ROR>
A;Cross-references: UNIPROT:Q12955; GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
C;Genetics:
A;Gene: GDB:ANK3
A;Cross-references: GDB:424503; OMIM:600465
A;Map position: 10q21-10q21
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C;Keywords: alternative splicing; peripheral membrane protein
F;73-105/Domain: ankyrin repeat homology <AN01>
F;106-138/Domain: ankyrin repeat homology <AN02>
F;139-171/Domain: ankyrin repeat homology <AN03>
F;172-200/Domain: ankyrin repeat homology <AN04>
F;201-233/Domain: ankyrin repeat homology <AN05>
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F;234-266/Domain: ankyrin repeat homology <AN06>
F;267-299/Domain: ankyrin repeat homology <AN07>
F;300-332/Domain: ankyrin repeat homology <AN08>
F;333-365/Domain: ankyrin repeat homology <AN09>
F;366-398/Domain: ankyrin repeat homology <AN10>
F;399-431/Domain: ankyrin repeat homology <AN11>
F;432-464/Domain: ankyrin repeat homology <AN12>
F;465-497/Domain: ankyrin repeat homology <AN13>
F;498-530/Domain: ankyrin repeat homology <AN14>
F;531-563/Domain: ankyrin repeat homology <AN15>
F;564-596/Domain: ankyrin repeat homology <AN16>
F;597-629/Domain: ankyrin repeat homology <AN17>
F;630-662/Domain: ankyrin repeat homology <AN18>
F;663-695/Domain: ankyrin repeat homology <AN19>
F;696-728/Domain: ankyrin repeat homology <AN20>
F;729-761/Domain: ankyrin repeat homology <AN21>
F;762-794/Domain: ankyrin repeat homology <AN22>
F;795-827/Domain: ankyrin repeat homology <AN23>

Query Match 8.8%; Score 377.5; DB 2; Length 4377;
Best Local Similarity 25.5%; Pred. No. 3.2e-13;
Matches 175; Conservative 92; Mismatches 277; Indels 141; Gaps 26;

Qy 184 TSGPVRDIADRIIVASKGDLSEDOVEILDIIFWES-----EIAEGISNPLH----- 230
Db 197 TKGKVRPLPALHIAARKDD-----TKAAALLQNDNADVESKSGFT-PLHIAAHYGNIN 249
Qy 231 -----ADVDDNPNVKGAKNVMTLMHLVYACDVPRIVKALGEVNDGDLGANAYNV 281
Db 250 VATLLNRAAAVDFT---ARNDDITPLH-VASKRGNANVVKLL-----LDRGAK-IDA 296
Qy 282 LDSSEGNPLHHAANKCTGDKLCKMEKTKTDFIDTANFANOSPLHIITQKPCDSCVLIDEE 341
Db 297 KTRDGLTPLHCGARSQHEQVEMLLDRAPILSKTKN--GLSPLHMAATQGDHLNVCVQL-- 352
Qy 342 FTSNLDPLGLVDGQKGNPLHHAHEHLPPVILKGMVDHVKNSSSEFQDLVNDPDYFGNTIAH 401
Db 353 LLQHNVPDVTNDYLTALHVAACHGHYKVAKVLLDCKANP-----NAKALNGFTPLH 405
Qy 402 YAVKKNADLTFLFNLKASGADLVNVRNVGSRPHVASNGKANANASGLVSCGIDVNSQD 461
Db 406 IACK-KNR-IKVMELLLKHGASIQAVTESGLTPIHVAAFMGHVNIIVSOLMHHGASPNVTN 463
Qy 462 VNGDTPPLHIAVEGSGMETVLAVLNQRGADVSQVNDGVTPLMSAAKYDIDIGVIAL--GS 519
Db 464 VRGETALHMAARSQAE-VVRYLVQDGAQVEAKAKDDQTPPLHISARLGKADIVQQLLQOG 522
Qy 520 AKPNI-----KGEDTVA-----KSLMEDYKGTPLHFAVAGGSRDTPR 558
Db 523 ASPNAATTSYTPPLHIAAREGHEDVAAFLDGHGASLSITTKGFTPLHVA----- 573
Qy 559 VVRKNYEKCHDLATIRAAALMDRSRGGELVNLGDPSESNILGSPNAKFLQHIQSANFGFSP 614
Db 574 -----KYGLEVANLLLOKSASPD-----AGKS 597
Qy 615 GSPARRGIVSSNNHVMKDILNFVGDLSLHLPSPERGYNAMQVAALFGDKEAVKMLAKSP 674
Db 598 GLTPLHVAHYDQKVALLLLD-QGASPHAAAKNGYTPPLHIAAKKNQMDIATSLLEYG-- 654
Qy 675 SDLNFKTSATPTPLNLAACLRGNEVVRGLVGQH-GIDINQRMGSDKNTVLHYVSKGDSF 733
Db 655 ADANAVTRQGIASVHLAAQEGHVDVMSVLLSRNANVNLNKSGL---TPLHLA-AQEDRV 710
Qy 734 LVOKILAHYDQVNCENNIGTPTPLHIAVEGGDPKIVSSLLKAGAVNRLDNGRSVLSSA 793
Db 711 NVAEVLVNOGAHVDAQTQMGYTPPLHVGHYGNIKIVNFIQLHSAKVNAKTKNGYTPALHQA 770
Qy 794 IVPRKEKGVILGVNKLDRGADIN 818
Db 771 -----AQQGTHIINVLQNNASPN 790

RESULT 11
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C:Genetics:

A;Note: DKFzp434D2328.1

Query Match 8.0%; Score 345; DB 2; Length 791;

Best Local Similarity 23.0%; Pred.No. 1.7e-12;

Matches 174; Conservative 110; Mismatches 275; Indels 196; Gaps 31;

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QY 228 PLHADVDNPNVKGAKNYM-----TLMLHLYACDVPDPRIVKALGEVDEGD 273
||| : : :
Db 6 PLHAASNGQINVVVKKLNLNGVEIDEINVYNTALHI--AC-----YNGQDAVNNELID 57
||| : : :
QY 274 LGANAVNLDSGNLPLHAAKNTGDKLCKLCKEYKTDIDT--ANFANQSPHIIITQK 331
||| : : :
Db 58 YGANV-NQPNNGNFTPLHFAAASHTG---ALCLLELVNNGADVNIQSKGKSPHMTAVH 113
||| : : :
QY 332 PDCSVLDIEFT--SRNL-----DFGLVDGDKGNPLHHAHPLPVILKGYM----- 376
||| : : :
Db 114 -----GRFTSRQTLQNGGEIDCVDKGNTPLHVAARYGHELLNITITSGADTAK 165
||| : : :
QY 377 -----DHVQNSSEFQDLVNDPDYFGNT 398
||| : : :
Db 166 GIHSMPFLHLAALNAHSDCCKLLSSGQKYSIVLSPNEHVL-SAGFE--IDTPDKFGRT 222
||| : : :
QY 399 IAHYAVKKNADITLFLNMLKASGADLNVRNVGAPIHVASSNGKANAVSGLVSCGIDVN 458
||| : : :
Db 223 CHHAAAAGGNVE--CIKLOSSGADPHKDKCGRTPLHYAAANGCHFHCIEITLVTTGANVN 280
||| : : :
QY 459 SDVNGDTPHLHIA-----VEGGMET-----VLAVLNORGADV 491
||| : : :
Db 281 ETDWGTALHYAASDMDRNKILNGAHNDSSELERARELKEATLCEFFLQNDANP 340
||| : : :
QY 492 SVQNDGVTPLMSAAKYG-----DIGVKA---LGSAPKNIKGEDT 529
||| : : :
Db 341 SIRDEKGYNSIHVAAAYGHRQCLELLERTNSGFEESDSGATKSPHLHAAVNGHQALEV 400
||| : : :
QY 530 VAKSLI---MEDYKGTPLHFVAGGSRDTRV-----VRKNYEK-----C 567
||| : : :
Db 401 LQSLVDLDRDEKGRALTDLAAFGHTECEBALINQASIFVKQDNVTKRTPLHASVING 460
||| : : :
QY 568 HDLATIRAALMQDRSGGELVNLGDFESENIL-----GSPNAKFLQHIQSAN-----FG 615
||| : : :
Db 461 HTLCL--RLLEIADNPEAVVDKAGQTPMLAVAYGHIDAVSLLEKEANVDVTDILG 518
||| : : :
QY 616 FSPARGIVSSNNHNMKDIILNFVGDLSLHLPSERGYNAMQVAALFGDKEAV-KMLAKSAPK 674
||| : : :
Db 519 CTALHGRIMTGHEECQMILLE-QEVSILCKDSRGRTPLHYAARGHATWLSLQWALSE 577
||| : : :
QY 675 SDLNFKTSATPTPLNLACLGDNNEVRLGVQGHGIDINQRMGSDKNTVLHYAISKGDSDL 734
||| : : :
Db 578 EDCFCFDNOGYTPLHWACVNGNENCIEVLLEQKCF---RKFIGNPETPLHCAIINDHGNC 634
||| : : :
QY 735 VQKILAHTGVD---VNCENNLGOTPLHLAVEGGDPKIVSSLLKAGAVNPLDDNGRSVLS 791
||| : : :
Db 635 ASLLIG--ADISSVCRDDKGRTPHAAAFADHVECLQLLRHSAPVNAVDSNGKIALM 692
||| : : :
QY 792 SAIVPRKXKGVILGIVNKLIDRG-ADINL-DGDHN 824
||| : : :
Db 693 MA-----AENGQAGAVDILLNSAQADLTVKDKDLN 722
||| : : :
```

RESULT 13

S11527

alpha-latrototoxin precursor - black widow spider

C:Species: Latrodectus mactans tredecimguttatus (black widow spider)

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-2004

C:Accession: S11527; JN0313

R:Kiyatkin, N.I.; Dulubova, I.E.; Chekhovskaya, I.A.; Grishin, E.V.

FEB5 Lett. 270, 127-131, 1990

A;Title: Cloning and structure of cDNA encoding alpha-latrototoxin from black widow spider

A;Reference number: S11527; MUID:91031994; PMID:1977615

A:Accession: S11527

A:Molecule type: mRNA

A:Residues: 1-1401 <KIY>

A;Cross-references: EMBL:X55009; NID:g9568; PIDN:CAA38753.1; PID:g9569
A;Note: it is uncertain whether Met-1, Met-8 or Met-18 is the initiator
R;Volkova, T.M.; Galkina, T.G.; Kudelin, A.B.; Grishin, E.V.
Bioorg. Khim. 17, 437-441, 1991
A;Title: tryptic fragments structure of the black widow spider venom neurotoxin.
A;Reference number: JN0313; MUID:91362695; PMID:1888339
A;Note: English title and abstract; article in Russian
A;Accession: JN0313

A:Molecule type: protein

A:Residues: 21-33 'X', 35-40 'X', 43-50, 82-90 'X', 92-99, 107-113, 114-126, 146-151, 171-178; 1

84-792, 881-891, 906-913, 914, 1015-1021, 1082-1065, 'X', 1067-1075, 1080-1084, 1087-1096, 1183-1

A;Note: the sequence of the amino terminal peptide has been corrected with tryptic pep

C;Superfamily: ankyrin repeat homology; EGF homology

C;Keywords: neurotoxin; venom

F;1-20/Domain: propeptide #status predicted <PRO>

F;21-1401/Product: alpha-latrototoxin #status experimental <MAT>

F;525-557/Domain: ankyrin repeat homology <AN7>

F;862-894/Domain: ankyrin repeat homology <AN3>

F;1005-1036/Domain: ankyrin repeat homology <AN21>

Query Match 8.0%; Score 344; DB 2; Length 1401;

Best Local Similarity 22.4%; Pred.No. 4.9e-12;

Matches 138; Conservative 97; Mismatches 207; Indels 174; Gaps 24;

```
QY 289 PLHAAKNCCTGDKLCKMCKTKTDFIDTANFANQSP-----LHIIT 329
||| : : :
Db 405 PVSUREKAC--PTLRMPVDQTRNVLFVRKFDSSKQLVGEITPYLSNFDIDRDLNAA 462
||| : : :
QY 330 QKPDSCVLDIEFTSNLDFGLVDGDKNPLHHAHPLPVILKGMVHVNSEFODLV 389
||| : : :
Db 463 SNPD-SAVGFKETKLY-----DGAN-----IRATFDH----- 490
||| : : :
QY 390 NDPDYFGNTIAHYAVKKNADITLFLNM-LKASGADLNVRNVGAPIHVASSNGKANAVS 448
||| : : :
Db 491 -----GRVFFHAAKSGN-DKIMFGLTFLAKSTELNQDKKGYTTPHVAADSGNAGIVN 543
||| : : :
QY 449 GLVSCGIDVNS-----QDVNGDTPHLHIAVE 473
||| : : :
Db 544 LLIQGVNSINSKYTHFLQTPHLAAQRGFVTTTQRLMESPEINERDKDGFPLHVAIR 603
||| : : :
QY 474 GSGMETVL-AVLNORGADVSQVNDGVTPLMSAAKYDGVVKA-LGSAPKNIKGEDTVA 531
||| : : :
Db 604 GG--ERILEAFNLQISIDVNAKSNLTGLTPFLHAIKNDWPVASTLLGSKKVDINAVDE-- 659
||| : : :
QY 532 KSLIMEDYKGFPLHFVAGGSRDTRFVRKNYEKCHDLATIRAALMQDRSGGELVNLGD 591
||| : : :
Db 660 -----NNITAHYAAAILGVLETK-----OLINLKE 685
||| : : :
QY 592 FSENLIGSPN-----AKFLOHIQSANF-----GFSPARRGIVSSNNH 629
||| : : :
Db 686 INA-NVVSFGLLSALHYAILYKHDDVASFLRSSNVNVLKALGITPLHLAVIQGRKQ 744
||| : : :
QY 630 VMKDILNFVGDLSLHLPSERGYNAMQVAALFGDKEAVKMLAKSAPKSDLNFKTSATPTPLN 689
||| : : :
Db 745 IL-SLMFDIGVNIQKTEKDEKTYPLHAAASKYKPELTIQLLDQO--SNFEAKTNSGATPLH 801
||| : : :
QY 690 LACLRGDNVVRGLVQGHGIDINQRMGSDKN--TVLHYAISKGDSDLVOKILAHTGVDVN 747
||| : : :
Db 802 LATTFKGSQAALILNN---EVNWR-DTDENGOMPIHGAAMTGLLDVAQAIIISIDATVVD 857
||| : : :
QY 748 CENNLGQTPHLHAVEGGDPKIVSSLLKAGAVNRLDDNGRSVLSSAIVPRKXKGVILGIV 807
||| : : :
Db 858 IEDKNSDTPNLAAQNSHDIVIKYFIDQGDADINTRNKKGLAPLAF-----SKKGNLDMV 912
||| : : :
QY 808 NKLLRGADINL-DGD 822
||| : : :
Db 913 KYLFQKNANVYIADND 928
||| : : :
```

RESULT 14

H71274

probable ankyrin - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: H71274
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: H71274
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-934 <COL>
A/Cross-references: UNIPROT:O83807; GB:AE001254; GB:AE000520; NID:g33323148; PIDN:AAC6580
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0835
C/Superfamily: syphilis spirochete probable ankyrin; ankyrin repeat homology
F:281-313/domain: ankyrin repeat homology <AN22>

Query Match 7.9%; Score 342; DB 1; Length 934;
Best Local Similarity 26.5%; Pred. No. 3.3e-12;
Matches 177; Conservative 85; Mismatches 241; Indels 166; Gaps 31;

QY 226 SNPLHADVNNPVKGA-----KNVM-----TLMLHLYACDVDPRIYKALGEVND 271
DB 283 ATPLHEAVRAGQVDAVLLRSGADPNVRDASGNTCLHLVAPAPPRVRLVGA 335
QY 272 GDGLANAYNVLSGNLPLHAAKCTGDKLCKEKTDF-----FDTANFANQSP 324
DB 336 LDAGASV-AIKODYGETPLHVA-----RLGMDRAFVERLVAGADISERNKGETP 386
QY 325 L-----HIITQKPCSVLDIEFT-----SRNL-----DFGLVDG-- 355
DB 387 LVLTIDRDHRLTAYFVSLGADIHAEDMRGETPLKALARGLETVKIVVTDNLYKQDVV 446
QY 356 GKNPLHVAEHLPPVILKGMVDRVNSSEFQDLVNDP-----DYFGNTIAHYAVKNKA 409
DB 447 GRDPLHVASR-----RAHLDIVK-----FLFREPKQMIARDTGMTNLLHYAVAND-- 492
QY 410 DLTFLNMLKASGADLNVRNVGRAPHYA--SSNGKANAVSLVSGGIDVNSQDVNGDTP 467
DB 493 DRAVGEFLMREGADIFSTNVHGVSPILKTALTTSGGRED-----WILTAANVHAQDTGNTP 548
QY 468 LHLAVEGSGMETVLAVLNORGADVSQVNDGVTPLMSAAKYGDIGVI----- 514
DB 549 LHLACEWKLTOAINGIL-RGAEIEARNLNQETPLFSAVKSDAAEVISILLHPQAGNPAL 607
QY 515 -----KALGSAKENIKGEDTVAKSL-MEDYKGFTHFVAGGSRD 555
DB 608 VDARDAVGNVTLHACVRMSALRSADVIREADARHVSLLNARNLSGKPLHLAARAGNV 667
QY 556 TFRVVRKNYEKCHDLATIPAAAL-MQDRSG-----GELVNLGDFESENILGSPNAKFLQHTQ 610
DB 668 FTRL-----LLSHRVALLHMGDETQKSAITDAVLADQESVHMLLSAGA---NPVQ 714
QY 611 SANFGSPARRGIVSSNNHNMVKDILNFVGDLSLHLPSERGYNAMQVAALFGDKEAVKMLAK 670
DB 715 QDMYGETPLHEAVLNCNSQSVIA-ALRAAGCNFPARDSYTTPLSLALLKGDTFVAGVCK 773
QY 671 SAKPSDLNFKTSATPTPLNLACLRGDNVEVRGLVQGHGIDINQRMGSKNTVLHYA 726
DB 774 -----DPLANSDGQTPHLAVM--ENVVPQTFRLLLAKGYPIDKDRMGS---SALVLA 823
QY 727 ISKGSFLVQKILAHGTGVNDVNCNNLGGTPLHLAVEGGDPKIVSLLK--AGAVNRLDD 784
DB 824 IKKORDLCHELLA-LGADLFTANNVGVSPALLVLSKN-----TSILKTLVGFVAVNKTDS 877
QY 785 NGRSVLSSA 793
DB 878 AGESILHYA 886

RESULT 15

Ti3940
ankylin - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: Ti3940
R:Dubreuil, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A/Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosop
A/Reference number: Z17820; MUID:95024098; PMID:7937942
A/Accession: Ti3940
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1549 <DUB>
A/Cross-references: UNIPROT:Q24241; EMBL:L35601; NID:g557083; PID:g557084; PIDN:AAC3720E
C/Genetics:
A/Cross-references: FlyBase:FBgn0011747

Query Match 7.9%; Score 339.5; DB 2; Length 1549;
Best Local Similarity 22.9%; Pred. No. 1.1e-11;
Matches 164; Conservative 100; Mismatches 249; Indels 203; Gaps 27;

QY 227 NPLHADVNNPVKGNVMTMLHLYACDVDPRIYKAL--GEVNDGDLGANAYNVLD 284
DB 22 NGMALDNKNGIKQNDATISFLAARSGDI-KKVMDFLDGCEI-SDIINSCNANGLNA--- 76
QY 285 EGNLPLHAAKNCCTGDKLCKMEKTKTDF-IDTANFANQSPHLHITQKPCSVLDIEFT 343
DB 77 -----LHLAAKQGVYD-----ICELLRRGIKIDNATKKNLHIAASLAGQHDVILQILY 128
QY 344 SRNLDGFLVDG-----DGKNPLHHAVEHLPPVILKGMVDRVKN 382
DB 129 NANNVQSLNGFTPLYMAAQENHNDCCRTLLANGANPSLSTEDGFTPLAVAMQGHDK-- 186
QY 383 SEFQDLVNDPDPFGNT---IAHYAVKNQADLTFLNMLKASGADLNVRNVGRAPHYA 439
DB 187 ---IVAVLLENDVRGKVRPLPALHIAAK-KN-DVNAKLLQLQHPNADIVSKSGFTPLHIAA 242
QY 440 SNGKANAVSLVSGGIDVNSQDVNGDTPHLHIAVEGSGMETVLAVLNORGADVSQVNDG 499
DB 243 HYGNDVIATLLNNKADVNYAKHMITPLHVACKWGKL-SLCTLLCCKGAKIDAAITRDL 301
QY 500 TPLMSAAKYGDIGVTK-----ALGSAKENIKGEDTVAKSLME----- 537
DB 302 TPLHCASRSGHVEVILKLLQGNAPILTKTKNGLSALHMAAQGEHDEAAHLLDNKAPVD 361
QY 538 -----DYK-----GFTPLHVFAGGSRDTFRVVRKN 563
DB 362 VTVDYLTALHVAACHGVKVAKLDDYKANPNARALNGFTPLHIAK-----KKN 410
QY 564 YEKCHDL-----ATIRAALMQDRSGELVNLGDFESENILGSPN--AKFLQHIQSANFG 616
DB 411 RIKVVELLIKGNANIGAT---TESGLTPLHVASF-----MGCINIVYLQHEASAD--- 459
QY 617 SPARGIVSSNNHNMVKDILNFVGDLSLHLPSERGYNAMQVAALFGDKEAVKMLAKSP 676
DB 460 -----LPTIRGETPLHAAARANQADIIRILRSKAVDA 492
QY 677 LNFKTSATPTPLNLACLRGDNVEVRGLVQGHGIDINQRMGSKNTVLHYAISKGSFLVQ 736
DB 493 I---VREGQTPHLVASRLGNINIIM-LLLQHGAEINAQ-SNDKYGALHIAAKEGQENIVQ 547
QY 737 KILAHGTGVNDVNCNNLGGTPLHLAVEGG----- 764
DB 548 -VLENGAENNAVTKGFTPLHLACKYQKNVQVLLONGASIDFQGNKDVTPPLHVATHY 606
QY 765 -DPKIVSLLKAGAYVNRLLDNGRSVLSSAIVPGRKRGVIGVKNKLDLDRGADINL 819
DB 607 NNPSIVELLKNGSSPNLCARNGQCAIHIAC-----KKNYLEIAMQLLQHGADVNI 657

Search completed: February 26, 2005, 18:54:50
Job time : 55 secs